

Genotype version 5.1.6
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MM nucleotide - nucleotide search, using SW model

Run on: August 13, 2003, 14:05:48 : Search time: 00:00:15 seconds

(with/out updates/sec)
1419/743 Million cell updates/sec

Title: US-10-009-962-1

Perfect score: 28

Sequence: 1 CCGTCGACAGCTTCTTACGTCGACATCACTT

Search table: IDENTITY_N90

Gapop 10.0 / Gapext 1.0

Searched: 2888711 seqs, 2045414386 positions

Total number of hits satisfying chosen parameters: 577712

Minimum hit seq length: 0

Maximum hit seq length: 2000000000

Post Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

```

Genbank: *
1: gb_ba: *
2: gb_ba: *
3: gb_in: *
4: gb_in: *
5: gb_in: *
6: gb_in: *
7: gb_in: *
8: gb_in: *
9: gb_in: *
10: gb_in: *
11: gb_in: *
12: gb_in: *
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16: gb_in: *
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18: gb_in: *
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32: gb_in: *
33: gb_in: *
34: gb_in: *
35: gb_in: *
36: gb_in: *
37: gb_in: *
38: gb_in: *
39: gb_in: *
40: gb_in: *
41: gb_in: *

```

Prod. No. is the number of results predicted by chosen database

Score directed hit of seqs. The score is the sum of the scores of the hits and the score of the hit is the sum of the scores of the hits.

2003/08/13

Result No.	Score	Query	Hit	Score	Query	Hit	Score	Query	Hit
1	20	100%	100%	20	100%	100%	20	100%	100%
2	19	100%	100%	19	100%	100%	19	100%	100%
3	19	100%	100%	19	100%	100%	19	100%	100%
4	19	100%	100%	19	100%	100%	19	100%	100%
5	19	100%	100%	19	100%	100%	19	100%	100%
6	19	100%	100%	19	100%	100%	19	100%	100%
7	19	100%	100%	19	100%	100%	19	100%	100%
8	19	100%	100%	19	100%	100%	19	100%	100%
9	19	100%	100%	19	100%	100%	19	100%	100%
10	19	100%	100%	19	100%	100%	19	100%	100%
11	19	100%	100%	19	100%	100%	19	100%	100%
12	19	100%	100%	19	100%	100%	19	100%	100%
13	19	100%	100%	19	100%	100%	19	100%	100%
14	19	100%	100%	19	100%	100%	19	100%	100%
15	19	100%	100%	19	100%	100%	19	100%	100%
16	19	100%	100%	19	100%	100%	19	100%	100%
17	19	100%	100%	19	100%	100%	19	100%	100%
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22	19	100%	100%	19	100%	100%	19	100%	100%
23	19	100%	100%	19	100%	100%	19	100%	100%
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36	19	100%	100%	19	100%	100%	19	100%	100%
37	19	100%	100%	19	100%	100%	19	100%	100%
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39	19	100%	100%	19	100%	100%	19	100%	100%
40	19	100%	100%	19	100%	100%	19	100%	100%
41	19	100%	100%	19	100%	100%	19	100%	100%
42	19	100%	100%	19	100%	100%	19	100%	100%
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45	19	100%	100%	19	100%	100%	19	100%	100%

2003/08/13

Result 1	A57648	100%	100%	100%	100%	100%	100%	100%	100%
A57648/c	A57648	100%	100%	100%	100%	100%	100%	100%	100%
DEFINITION	Sequence of the human gene, full length.								
VERSION	A57648.1								
KEYWORDS	Sequence of the human gene, full length.								
ORIGIN	1								
DEFINITION	Sequence of the human gene, full length.								
VERSION	A57648.1								
KEYWORDS	Sequence of the human gene, full length.								
ORIGIN	1								
DEFINITION	Sequence of the human gene, full length.								
VERSION	A57648.1								
KEYWORDS	Sequence of the human gene, full length.								
ORIGIN	1								

[illegible]

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Y. H. L. & J. H. L.

WILLIAM A. VANDERKAM

[illegible]

K₁⁺, K₂⁺, K₃⁺, K₄⁺, K₅⁺, K₆⁺, K₇⁺, K₈⁺, K₉⁺, K₁₀⁺, K₁₁⁺, K₁₂⁺, K₁₃⁺, K₁₄⁺, K₁₅⁺, K₁₆⁺, K₁₇⁺, K₁₈⁺, K₁₉⁺, K₂₀⁺, K₂₁⁺, K₂₂⁺, K₂₃⁺, K₂₄⁺, K₂₅⁺, K₂₆⁺, K₂₇⁺, K₂₈⁺, K₂₉⁺, K₃₀⁺, K₃₁⁺, K₃₂⁺, K₃₃⁺, K₃₄⁺, K₃₅⁺, K₃₆⁺, K₃₇⁺, K₃₈⁺, K₃₉⁺, K₄₀⁺, K₄₁⁺, K₄₂⁺, K₄₃⁺, K₄₄⁺, K₄₅⁺, K₄₆⁺, K₄₇⁺, K₄₈⁺, K₄₉⁺, K₅₀⁺, K₅₁⁺, K₅₂⁺, K₅₃⁺, K₅₄⁺, K₅₅⁺, K₅₆⁺, K₅₇⁺, K₅₈⁺, K₅₉⁺, K₆₀⁺, K₆₁⁺, K₆₂⁺, K₆₃⁺, K₆₄⁺, K₆₅⁺, K₆₆⁺, K₆₇⁺, K₆₈⁺, K₆₉⁺, K₇₀⁺, K₇₁⁺, K₇₂⁺, K₇₃⁺, K₇₄⁺, K₇₅⁺, K₇₆⁺, K₇₇⁺, K₇₈⁺, K₇₉⁺, K₈₀⁺, K₈₁⁺, K₈₂⁺, K₈₃⁺, K₈₄⁺, K₈₅⁺, K₈₆⁺, K₈₇⁺, K₈₈⁺, K₈₉⁺, K₉₀⁺, K₉₁⁺, K₉₂⁺, K₉₃⁺, K₉₄⁺, K₉₅⁺, K₉₆⁺, K₉₇⁺, K₉₈⁺, K₉₉⁺, K₁₀₀⁺, K₁₀₁⁺, K₁₀₂⁺, K₁₀₃⁺, K₁₀₄⁺, K₁₀₅⁺, K₁₀₆⁺, K₁₀₇⁺, K₁₀₈⁺, K₁₀₉⁺, K₁₁₀⁺, K₁₁₁⁺, K₁₁₂⁺, K₁₁₃⁺, K₁₁₄⁺, K₁₁₅⁺, K₁₁₆⁺, K₁₁₇⁺, K₁₁₈⁺, K₁₁₉⁺, K₁₂₀⁺, K₁₂₁⁺, K₁₂₂⁺, K₁₂₃⁺, K₁₂₄⁺, K₁₂₅⁺, K₁₂₆⁺, K₁₂₇⁺, K₁₂₈⁺, K₁₂₉⁺, K₁₃₀⁺, K₁₃₁⁺, K₁₃₂⁺, K₁₃₃⁺, K₁₃₄⁺, K₁₃₅⁺, K₁₃₆⁺, K₁₃₇⁺, K₁₃₈⁺, K₁₃₉⁺, K₁₄₀⁺, K₁₄₁⁺, K₁₄₂⁺, K₁₄₃⁺, K₁₄₄⁺, K₁₄₅⁺, K₁₄₆⁺, K₁₄₇⁺, K₁₄₈⁺, K₁₄₉⁺, K₁₅₀⁺, K₁₅₁⁺, K₁₅₂⁺, K₁₅₃⁺, K₁₅₄⁺, K₁₅₅⁺, K₁₅₆⁺, K₁₅₇⁺, K₁₅₈⁺, K₁₅₉⁺, K₁₆₀⁺, K₁₆₁⁺, K₁₆₂⁺, K₁₆₃⁺, K₁₆₄⁺, K₁₆₅⁺, K₁₆₆⁺, K₁₆₇⁺, K₁₆₈⁺, K₁₆₉⁺, K₁₇₀⁺, K₁₇₁⁺, K₁₇₂⁺, K₁₇₃⁺, K₁₇₄⁺, K₁₇₅⁺, K₁₇₆⁺, K₁₇₇⁺, K₁₇₈⁺, K₁₇₉⁺, K₁₈₀⁺, K₁₈₁⁺, K₁₈₂⁺, K₁₈₃⁺, K₁₈₄⁺, K₁₈₅⁺, K₁₈₆⁺, K₁₈₇⁺, K₁₈₈⁺, K₁₈₉⁺, K₁₉₀⁺, K₁₉₁⁺, K₁₉₂⁺, K₁₉₃⁺, K₁₉₄⁺, K₁₉₅⁺, K₁₉₆⁺, K₁₉₇⁺, K₁₉₈⁺, K₁₉₉⁺, K₂₀₀⁺, K₂₀₁⁺, K₂₀₂⁺, K₂₀₃⁺, K₂₀₄⁺, K₂₀₅⁺, K₂₀₆⁺, K₂₀₇⁺, K₂₀₈⁺, K₂₀₉⁺, K₂₁₀⁺, K₂₁₁⁺, K₂₁₂⁺, K₂₁₃⁺, K₂₁₄⁺, K₂₁₅⁺, K₂₁₆⁺, K₂₁₇⁺, K₂₁₈⁺, K₂₁₉⁺, K₂₂₀⁺, K₂₂₁⁺, K₂₂₂⁺, K₂₂₃⁺, K₂₂₄⁺, K₂₂₅⁺, K₂₂₆⁺, K₂₂₇⁺, K₂₂₈⁺, K₂₂₉⁺, K₂₃₀⁺, K₂₃₁⁺, K₂₃₂⁺, K₂₃₃⁺, K₂₃₄⁺, K₂₃₅⁺, K₂₃₆⁺, K₂₃₇⁺, K₂₃₈⁺, K₂₃₉⁺, K₂₄₀⁺, K₂₄₁⁺, K₂₄₂⁺, K₂₄₃⁺, K₂₄₄⁺, K₂₄₅⁺, K₂₄₆⁺, K₂₄₇⁺, K₂₄₈⁺, K₂₄₉⁺, K₂₅₀⁺, K₂₅₁⁺, K₂₅₂⁺, K₂₅₃⁺, K₂₅₄⁺, K₂₅₅⁺, K₂₅₆⁺, K₂₅₇⁺, K₂₅₈⁺, K₂₅₉⁺, K₂₆₀⁺, K₂₆₁⁺, K₂₆₂⁺, K₂₆₃⁺, K₂₆₄⁺, K₂₆₅⁺, K₂₆₆⁺, K₂₆₇⁺, K₂₆₈⁺, K₂₆₉⁺, K₂₇₀⁺, K₂₇₁⁺, K₂₇₂⁺, K₂₇₃⁺, K₂₇₄⁺, K₂₇₅⁺, K₂₇₆⁺, K₂₇₇⁺, K₂₇₈⁺, K₂₇₉⁺, K₂₈₀⁺, K

[illegible]

THE UNIVERSITY OF CHICAGO

Figure 1 illustrates the experimental setup. A subject is seated at a table, viewing a video screen. A camera is positioned above the screen. A target is placed on the table. A horizontal arrow indicates the direction of movement. A vertical arrow indicates the direction of the video feedback. A dashed line indicates the path of the hand. A solid line indicates the path of the video feedback. A legend indicates that the solid line represents the video feedback and the dashed line represents the hand path.

Figure 1 shows a Western blot analysis of p38 phosphorylation in various tissues. The tissues analyzed are Brain, Liver, Kidney, Heart, Muscle, and Adipose. The conditions are Control, LPS, LPS+SB, and LPS+SB+P. The blot shows p38 protein levels, with phosphorylation indicated by a shift in the band position. Molecular weight markers are shown on the left.

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[illegible]

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[illegible]

Figure 1 illustrates the experimental setup. A subject is seated at a table, viewing a video screen. A camera is positioned above the screen. A light source is positioned to the left of the screen. A subject is seated at a table, viewing a video screen. A camera is positioned above the screen. A light source is positioned to the left of the screen. A subject is seated at a table, viewing a video screen. A camera is positioned above the screen. A light source is positioned to the left of the screen.

[illegible]

Table 1. *Continued*

[illegible]

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[illegible]

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

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The diagram illustrates the experimental setup for studying the effect of the initial concentration of the polymer solution on the morphology of the polymer film. It shows a cross-section of a polymer film on a substrate. The film is divided into two main regions: a top region labeled 'Polymer solution' and a bottom region labeled 'Substrate'. The top region is further divided into two sub-regions: 'Polymer solution' and 'Polymer solution'. The bottom region is labeled 'Substrate'. The diagram illustrates the process of polymerization and the resulting morphology of the polymer film.

100

Genotype version 5.1.4
Copyright (c) 1993 - 2003 Computer 11.1

OM nucleotide - nucleotide search, using SW model

Run on: August 13, 2003, 19:05:48 : Search time 00:01:17 seconds

(without alignment)
1419/748 Million overlapped bases/sec

Title: US-10-009-962-2

Perfect score: 28

Sequence: 1 CCGTGACCTTAAGAAACCTTCGACAGG 28

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Search: 2388711 seqs, 2545481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 99
Maximum Match 100%

Listing first 45 summaries

Database: Genbank
1: qb_ba:*
2: qb_ba:*
3: qb_ba:*
4: qb_ba:*
5: qb_ba:*
6: qb_ba:*
7: qb_ba:*
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32: qb_ba:*
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35: qb_ba:*
36: qb_ba:*
37: qb_ba:*
38: qb_ba:*
39: qb_ba:*
40: qb_ba:*
41: qb_ba:*

Prod. No. is the number of results predicted by database

Score greater than or equal to the score of the best hit is shown
and is reported by database. The score is reported by database.

SUMMARY

Result No.	Score	Query Match	Length	Pos	Hit
1	28	100%	28	1	AV120681
2	28	100%	28	1	AV120681
3	28	100%	28	1	AV120681
4	28	100%	28	1	AV120681
5	28	100%	28	1	AV120681
6	28	100%	28	1	AV120681
7	28	100%	28	1	AV120681
8	28	100%	28	1	AV120681
9	28	100%	28	1	AV120681
10	28	100%	28	1	AV120681
11	28	100%	28	1	AV120681
12	28	100%	28	1	AV120681
13	28	100%	28	1	AV120681
14	28	100%	28	1	AV120681
15	28	100%	28	1	AV120681
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18	28	100%	28	1	AV120681
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39	28	100%	28	1	AV120681
40	28	100%	28	1	AV120681
41	28	100%	28	1	AV120681

REFERENCE

1. AV120681
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SUBJECT: ...

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TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 219615)
AUTHORS Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Human Genome Sequencing Project, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
1 (bases 1 to 219615)
REFERENCE Direct Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (19-NOV-2002) Human Genome Sequencing Project, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

29-Nov-02, 2002 This sequence section contains a draft assembly of the sequence in this assembly is a combination of raw-based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/atlas/>). Each of the reads in the feature table below represents a scaffold in the Atlas assembly (a "contig-scaffold") within each contig-scaffold individual sequence reads are ordered and oriented and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clones and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GHS
Center clone name: CH220.205021

Summary Statistics
Assembly program: Phrap; Version: 2.99.27
Consensus quality: 186890 bases at least Q40
Consensus quality: 190576 bases at least Q50
Consensus quality: 192814 bases at least Q20
Estimated insert size: 194492; sum-of-contigs estimation
Quality coverage: 100% in 220 bases; average coverage: 100% in 220 bases

* NOTE: Estimated insert size may differ from sequence length
* (see <http://www.hgsc.bcm.tmc.edu/ftp/seq/seq.html>)
* NOTE: This is a working draft sequence; it currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 216312: contig of 216312 bp in length
* 216311 216412: gap of unknown length
* 216411 216722: contig of 1260 bp in length
* 216721 217772: gap of unknown length
* 217771 219615: contig of 1863 bp in length

FEATURES
source
1..219615
Location/Qualifiers
1..219635
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH220.205021"

Misc-feature

BASE COUNT 55574 A 43247 C 44777 G 51145 T 20992 Others
ORIGIN

Query Match 70.0%; Score 19.6; HB 2; Length 219615;
Best Local Similarity 84.5%; Prod. No. 4,50,02;
Matches 22; Conservative 0; Mismatches 4; Gaps 0

UY
ID
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
REFERENCE
AUTHORS

1 (bases 1 to 219615)
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 219615)
AUTHORS Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Human Genome Sequencing Project, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
1 (bases 1 to 219615)
REFERENCE Direct Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (19-NOV-2002) Human Genome Sequencing Project, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
29-Nov-02, 2002 This sequence section contains a draft assembly of the sequence in this assembly is a combination of raw-based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/atlas/>). Each of the reads in the feature table below represents a scaffold in the Atlas assembly (a "contig-scaffold") within each contig-scaffold individual sequence reads are ordered and oriented and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clones and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

TITLE
JOURNAL

COMMENT
Submitted (05-Sep-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 5, 2002 this sequence version replaced all previous
All repeats were identified using RepeatMasker
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.ncbi.nlm.nih.gov/pub/1000000000

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIMR
Web site: <http://www.seq.wimr.edu>
Contact: sequence.submissions@wimr.edu

Project Information

Center project name: L2917

Center clone name: 6_P-5

Summary Statistics

Sequencing vector: M13, M79915; 499 of reads

Sequencing vector: Plasmid: 5/31 514 of reads

Chemistry: Dye-terminator BigDye 1.0/1.0/1.0

Assembly program: Phrap; version 0.960731

Consensus quality: 151639 bases at least 90

Consensus quality: 152571 bases at least 920

Insert size: 16700; average 16

Insert size: 16787; sum-of-cons 15

Quality coverage: 10.1 in 920 bases; average 16

Quality coverage: 10.8 in 920

NOTE: This is a "working draft" sequence. It currently

consists of 5 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1 16710: contig of 16710 bp in length

16711 16810: gap of 100 bp

16811 20475: contig of 3665 bp in length

20376 20475: gap of 100 bp

20476 40856: contig of 20380 bp in length

40856 40856: gap of 100 bp

40956 100466: contig of 59411 bp in length

100466 100466: gap of 100 bp

100467 153187: contig of 52721 bp in length

153187 153187: contig of 52721 bp in length

Location: GenBank

1. 153187

Organism: "Homo sapiens"

mol_type: "genomic DNA"

db_xref: "taxon:9606"

chromosome: "20"

map: "20"

clone: "Rp11-6p5"

/clone.lib: "RP11-11 Human Male BAC"

1. 16710

/note: "assembly fragment"

clone_end: "Spb"

vector_side: "left"

16811. 20475

/note: "assembly fragment"

20476. 40856

misc_feature

misc_feature

misc_feature

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DEFINITION

Homo sapiens chromosome 17, and the part of the map of the Working Draft Human Genome Project (HGP) located on the short arm of chromosome 17.

SYNOPSIS

11p15.5

KEYWORDS

11p15.5

REFERENCES

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11p15.5

REFERENCES

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11p15.5

Count length
 Average values in est (unit)
 Average error rate (from phage estimation)
 Fraction of phage above loss than 10
 Number of phage above loss than 10
 Number of N's in a sequence

Position
 20384
 25298
 59226
 66011
 66014
 66015
 54039
 54826
 63371

Length (base pair) 1 2000 4 1 10000
 10001
 9001
 8001
 7001
 6001
 5001
 4001
 3001
 2001
 1001
 01

Position
 20384
 25298
 59226
 66011
 66014
 66015
 54039
 54826
 63371

Count length
 Average values in est (unit)
 Average error rate (from phage estimation)
 Fraction of phage above loss than 10
 Number of phage above loss than 10
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 63371

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 66015
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 54826
 63371

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 12, 2003, 19:05:18, Search time 749.185 seconds

(without alignments)
1419 743 million coil updates/sec

Title: US-10-009-962-4

Perfect score: 26

Sequence: 1 GGTTCGAACTGCTAGCTGAAATTAATGC 26

Scoring table:

IDENTITY MRC
GAPOP 10.0, GAPEXT 1.0

Searched: 2888711 seqs, 20154912384 residues

Total number of hits satisfying chosen parameters: 5777122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenEmbl:
1: gb_ba:
2: gb_bhg:
3: gb_in:
4: gb_om:
5: gb_oy:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vl:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:
29: em_vl:
30: em_htg_hum:
31: em_htg_in:
32: em_htg_other:
33: em_htg_mus:
34: em_htg_plu:
35: em_htg_rca:
36: em_htg_man:
37: em_htg_vrl:
38: em_sy:
39: em_hlgo_hum:
40: em_hlgo_mus:
41: em_hlgo_other:

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being displayed
and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Quality	Match Length (bp)	ID	Accession	Source
1	19.6	75.4	12795	2	AF022835	GenBank
2	19.6	75.4	12795	2	AF022835	GenBank
3	18.6	71.5	84705	2	AF022835	GenBank
4	18.6	71.5	84705	2	AF022835	GenBank
5	18.6	71.5	84705	2	AF022835	GenBank
6	18.6	71.5	84705	2	AF022835	GenBank
7	18.6	71.5	84705	2	AF022835	GenBank
8	18.6	71.5	84705	2	AF022835	GenBank
9	18.6	71.5	84705	2	AF022835	GenBank
10	18.6	71.5	84705	2	AF022835	GenBank
11	18.6	71.5	84705	2	AF022835	GenBank
12	18.6	71.5	84705	2	AF022835	GenBank
13	18.6	71.5	84705	2	AF022835	GenBank
14	18.6	71.5	84705	2	AF022835	GenBank
15	18.6	71.5	84705	2	AF022835	GenBank
16	18.6	71.5	84705	2	AF022835	GenBank
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18	18.6	71.5	84705	2	AF022835	GenBank
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40	18.6	71.5	84705	2	AF022835	GenBank
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42	18.6	71.5	84705	2	AF022835	GenBank
43	18.6	71.5	84705	2	AF022835	GenBank
44	18.6	71.5	84705	2	AF022835	GenBank
45	18.6	71.5	84705	2	AF022835	GenBank

ALL HITS

Result No.	Score	Quality	Match Length (bp)	ID	Accession	Source
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44	18.6	71.5	84705	2	AF022835	GenBank
45	18.6	71.5	84705	2	AF022835	GenBank

[illegible]

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

(HMOs: All but one in) (from 1-1000);
and 100% of MAS, FMM, and PMA were

DOI: 10.1002/anie.200600000

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Journal of Management Education 30(6)br/>© The Author(s)
10.1177/0095647206289111
<http://jme.sagepub.com>

1. *Phragmites australis* (Cav.) Trin. ex Steud. (Common reed)

[illegible]

1. *Introduction*
 2. *Methodology*
 3. *Results*
 4. *Discussion*
 5. *Conclusion*
 6. *References*
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 234. *Tables*
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 236. *Supplementary Materials*
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 239. *Acknowledgments*
 240. *References*
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[illegible]

1. The first step is to identify the key components of the system. This involves understanding the hardware, software, and data involved in the process.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	

Modelo de Equações em Latentes (MEQL) (Jöreskog, 1993). Este modelo permite avaliar a validade dos construtos e a validade das hipóteses propostas. Os resultados da análise de validade dos construtos são apresentados na Tabela 1.

1. $\mathcal{A} = \{A_1, A_2, \dots, A_n\}$ is a family of n sets.
 2. \mathcal{A} is a σ -algebra if:
 (a) $A \in \mathcal{A} \implies A^c \in \mathcal{A}$ (closed under complementation).
 (b) $A_1, A_2, \dots \in \mathcal{A} \implies \bigcup_{i=1}^{\infty} A_i \in \mathcal{A}$ (closed under countable unions).
 (c) $A_1, A_2, \dots \in \mathcal{A} \implies \bigcap_{i=1}^{\infty} A_i \in \mathcal{A}$ (closed under countable intersections).
 (d) $\emptyset \in \mathcal{A}$ and $X \in \mathcal{A}$.

[illegible]

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[illegible]

Figure 1. The relationship between the number of species and the number of genera in the family *Ascomycetaceae*.

11.

10

$$Z = 1$$

10

100

10. $\frac{1}{2}$

$$\frac{1}{2} \mathbf{Z}$$

1. $\frac{1}{2}$

[illegible]

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1. The authors are indebted to the National Science Foundation for the award of a grant to support this work.

1. For each solution \mathbf{u} in \mathcal{S}_1 , we select a $\mathbf{v} \in \mathcal{S}_2$ such that $\mathbf{u} \cdot \mathbf{v} = 1$. We then project \mathbf{v} onto the plane $\Pi_{\mathbf{u}}$ and obtain \mathbf{v}' . All vectors associated with \mathbf{u} are then projected onto $\Pi_{\mathbf{u}}$ and \mathbf{v}' is added to \mathcal{S}_1 . A P.A. is then selected from \mathcal{S}_1 and \mathcal{S}_2 is updated by adding \mathbf{v}' to \mathcal{S}_2 .

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Center	Washington University Genome Sequencing Center
Center web	WGCSC
Web site	http://www.wustl.edu/genom/
Project Information	
Center project name	H_M0205012
Summary Statistics	
Sequencing vector	M13, 73%
Sequencing method	plasmid, 97%
Chemistry	Dye-terminator ET, 73% of reads
Chemistry	Dye-terminator ET, 27% of reads
Assembly program	Phrap, version 0.990016
Consensus quality	167798 bases at least Q40
Consensus quality	171101 bases at least Q30
Consensus quality	177282 bases at least Q20
Insert size	187000; agarose-rip
Insert size	176197; sum-of-coverage
Quality coverage	2.54 in Q20 bases, 343060 bp
Quality coverage	4.10 in Q20 bases, 3400000 bp
<p>NOTE: This is a working draft sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.</p>	
1	1477: contig of 1477 bp in length
1478	1577: gap of unknown length
1578	3566: contig of 1989 bp in length
3567	3666: gap of unknown length
3667	5440: contig of 1774 bp in length
5441	5540: gap of unknown length
5541	8092: contig of 2552 bp in length
8093	8192: gap of unknown length
8193	10790: contig of 2607 bp in length
10800	10890: gap of unknown length
10900	16410: contig of 5511 bp in length
16411	16510: gap of unknown length
16511	21762: contig of 5252 bp in length
21763	21862: gap of unknown length
21863	27079: contig of 5216 bp in length
27079	27179: gap of unknown length
27179	33120: contig of 5042 bp in length
33121	33220: gap of unknown length
33221	39122: contig of 4252 bp in length
39123	39572: gap of unknown length
39573	48260: contig of 3689 bp in length
48261	48360: gap of unknown length
48361	56756: contig of 6355 bp in length
56757	56856: gap of unknown length
56857	65334: contig of 9278 bp in length
65335	65434: gap of unknown length
65435	75670: contig of 10236 bp in length
75671	75770: gap of unknown length
75771	87026: contig of 11256 bp in length
87027	87126: gap of unknown length
87127	99477: contig of 12951 bp in length
99478	99577: gap of unknown length
99578	111227: contig of 11550 bp in length

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Genodex version 5.1.6
Copyright (c) 1993 - 2003 Genodex Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2003, 21:17:00; Search time 174.711 seconds
(with both alignments)

432.951 Million read updates/sec

Title: US-10-009-962-1

Perfect score: 28

Sequence: 1 CCGTCAGAAAGCTTCTTAAGATCAGATG 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1449719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 09

Listing first 45 summaries

```
Database: R-Geneset_1000000000
1: 5105512 hits found in the database
2: 5105512 hits found in the database
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25: 5105512 hits found in the database
```

Pred. No. is the number of results predicted by query. The lower
score greater than or equal to the score of the result point printed
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Accession
1	19.6	70.0	245	ABX27005
2	19.6	70.0	251	ABX27014
3	19.6	70.0	278	ABX31436
4	19.6	70.0	2453	AAQ47606
5	19.6	70.0	7142	AAQ47606
6	19.2	68.6	40	AAQ47606
7	19.2	68.6	3096	AAQ47606
8	19.2	68.6	5434	AAQ47606

9	19.2	68.6	2127	AAQ47606
10	19.2	68.6	7122	AAQ47606
11	19	68.6	1000	AAQ47606
12	19	68.6	1000	AAQ47606
13	18.8	68.6	1000	AAQ47606
14	18.8	68.6	1000	AAQ47606
15	18.8	68.6	1000	AAQ47606
16	18.8	68.6	1000	AAQ47606
17	18.8	68.6	1000	AAQ47606
18	18.8	68.6	1000	AAQ47606
19	18.8	68.6	1000	AAQ47606
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21	18.8	68.6	1000	AAQ47606
22	18.8	68.6	1000	AAQ47606
23	18.8	68.6	1000	AAQ47606
24	18.8	68.6	1000	AAQ47606
25	18.8	68.6	1000	AAQ47606
26	18.8	68.6	1000	AAQ47606
27	18.8	68.6	1000	AAQ47606
28	18.8	68.6	1000	AAQ47606
29	18.8	68.6	1000	AAQ47606
30	18.8	68.6	1000	AAQ47606
31	18.8	68.6	1000	AAQ47606
32	18.8	68.6	1000	AAQ47606
33	18.8	68.6	1000	AAQ47606
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40	18.8	68.6	1000	AAQ47606
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43	18.8	68.6	1000	AAQ47606
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46	18.8	68.6	1000	AAQ47606
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100	18.8	68.6	1000	AAQ47606

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100 0000 1140

therapy. It can also be used to repopulate blood cells in a mammal.
 CC The products can also be used to treat, e.g., neoplastic disorders,
 CC arteriosclerosis, type II diabetes, polycystic ovarian disease,
 CC cardiovascular diseases, osteoarthritis, demyelinating disorders,
 CC hypertension, insulin resistance, hypercholesterolemia,
 CC hypertriglyceridemia, cancer and cholesterol-lowering.
 XX
 SO Sequence 7127 BP; 1683 A; 1691 G; 1859 G; 1654 T; 0 other
 Query Match 68.6%; Score 19.7; NP 1%; Length 7127;
 Best Local Similarity 87.5%; Pred. No. 91;
 Matches 21; Conservation 0; Mismatches 2; Totals 0; Gaps 0
 OY 3 CTCGAGAGCTTCTAAGCTGAG 26
 DB 0101 CTCGAGAGCTTCTGAGCTGAG 2128
 RESULT 10
 AA175093/5
 ID AA175093 standard; DNA: 7127 BP.
 XX
 AC AA175093;
 XX
 DI 07-09T-1997 (first entry)
 DE Human obesity: Fitchell, J. Hum. 1991 280CH3 gene 1.0.0.
 XX
 KW Obesity: protein: ob protein; 1991; 1015-1150; bolina; 1991;
 KW weight loss; appetite loss; anorexia; emphysema; hypercholesterolemia; ob.
 XX
 OS Chimeric Homo sapiens;
 OS Chimeric bacteriophage Sp6;
 OS Chimeric SV40 virus;
 OS Chimeric herpes simplex virus;
 OS Chimeric bacteriophage M13.
 XX
 FH Key Location/Qualifiers
 FT misc_RNA 612
 FT /note= "PNA start"
 FT 776..844
 FT /tag= b
 FT /note= "Sp6 promoter"
 FT 845
 FT /tag= c
 FT /note= "Sp6 RNA start"
 FT 918..2112
 FT /tag= d
 FT /note= "Chimeric
 FT 2183
 FT /tag= e
 FT /note= "SV40 early polyA"
 FT 2324
 FT /tag= f
 FT /note= "SV40 origin"
 FT 2748
 FT /tag= g
 FT /note= "polyA start"
 FT 2756..2891
 FT /tag= h
 FT /note= "7x promoter"
 FT 2892..3892
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 FT 3893
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 FT 4526..4643
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 FT 4645
 FT /tag= l
 FT misc_RNA

FT /note= "pDR22 sequence"
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 XX W3724444 A1
 XX 10-JUL-1997
 XX 19-DEC-1996 9608-0520738
 XX 20-JUN-1996 9608-0627184
 XX 27-DEC-1995 9608-0629494
 XX (CERN) GENBANK 1997
 XX DE Sauvage M, Leclerc N, Vaudry H
 XX 14-1997 0629494
 XX P-PSDB: AAW22722
 XX
 XX Obesity: ob; Protein deficiencies; with extended half life; used
 XX to induce weight or appetite loss; or treat obesity; polycystic
 XX diabetes
 XX
 XX Example 1: Page 24-29; 1997; 1015-1150
 XX
 XX A PNA construct (AA175093) includes a coding sequence for an ob
 XX chimeric (AA175093) comprising the full-length human obesity (ob)
 XX protein and human polyA signal and a PNA domain, ob-PNA, and
 XX by PCR amplification of the full-length ob and PNA RNA and PNA
 XX and subcloned into vector pCR2.1 (see Example 1). The ob-PNA
 XX can be expressed in transformed host cells. It has an expected
 XX half-life compared to native ob protein and can be used to
 XX weight or appetite loss, to treat obesity, bolina, or
 XX diabetes; to induce growth of a hyper-obesity cells; and
 XX treat kidney ailments, hypertension and other disorders such as
 XX emphysema.
 XX
 SO Sequence 7127 BP; 1683 A; 1691 G; 1859 G; 1654 T; 0 other
 Query Match 68.6%; Score 19.7; NP 1%; Length 7127;
 Best Local Similarity 87.5%; Pred. No. 91;
 Matches 21; Conservation 0; Mismatches 2; Totals 0; Gaps 0
 OY 3 CTCGAGAGCTTCTAAGCTGAG 26
 DB 0101 CTCGAGAGCTTCTGAGCTGAG 2128
 RESULT 11
 AA175093/5
 ID AA175093 standard; DNA: 7127 BP.
 XX
 AC AA175093;
 XX
 DI 15-AUG-2002 (first entry)
 DE Bacterial bacteriophage genome sequence for (S1) 4.2.2.
 XX
 KW Bacterial bacteriophage genome sequence for (S1) 4.2.2.
 KW altered culture condition; 0.1% formaldehyde; 100%
 KW Physiological processes; ob.
 XX
 XX Bacterial bacteriophage genome sequence for (S1) 4.2.2.
 XX 11-AUG-2002
 XX 05-09T-2002 2002-05-09T-2002
 XX 06-09T-2002 2002-06-09T-2002
 XX 27-MAR-2001 2001-03-27T-2001



[illegible]

The first correlation between the studied parameters and the production of infective oocysts was found in the first step of the model of development in the host, and it was significant ($P < 0.001$) in all cases. The second correlation was found in the third step of the model of development, that is, in the presence of a host that does not eliminate the oocysts (CM1, CM2, CM3, CM4, CM5, CM6, CM7, CM8, CM9, CM10, CM11, CM12, CM13, CM14, CM15, CM16, CM17, CM18, CM19, CM20, CM21, CM22, CM23, CM24, CM25, CM26, CM27, CM28, CM29, CM30, CM31, CM32, CM33, CM34, CM35, CM36, CM37, CM38, CM39, CM40, CM41, CM42, CM43, CM44, CM45, CM46, CM47, CM48, CM49, CM50, CM51, CM52, CM53, CM54, CM55, CM56, CM57, CM58, CM59, CM60, CM61, CM62, CM63, CM64, CM65, CM66, CM67, CM68, CM69, CM70, CM71, CM72, CM73, CM74, CM75, CM76, CM77, CM78, CM79, CM80, CM81, CM82, CM83, CM84, CM85, CM86, CM87, CM88, CM89, CM90, CM91, CM92, CM93, CM94, CM95, CM96, CM97, CM98, CM99, CM100).

the same as the one used in the previous study. The same data were used for the present study, but the data were re-analyzed to determine if the same pattern of results could be replicated. The same data were also re-analyzed to determine if the same pattern of results could be replicated. The same data were also re-analyzed to determine if the same pattern of results could be replicated.

[illegible][illegible][illegible]

Category	Count
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98	10
99	10
100	10

$$\begin{array}{ll} \text{I} & \hat{A}(t); \quad t \in [0, T] \\ \text{XX} & \text{Stochastic}; \quad \sigma^2 \neq 0; \quad t \geq 0 \\ A^{**} & \hat{A}(t); \quad t \in [0, T]; \end{array}$$
[illegible]

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

[illegible]

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[illegible]
$$N_{\text{eff}} = 3.36 \pm 0.11 \text{ (stat)} \pm 0.07 \text{ (sys)}$$

Veroff, J., Douvan, E., & Kuk, J. (1996). *Adolescent development: A life-span perspective*. Mahwah, NJ: Lawrence Erlbaum Associates, Inc.

[illegible]

1. $\frac{1}{2}$
 2. $\frac{1}{3}$
 3. $\frac{1}{4}$
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 5. $\frac{1}{6}$
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1. Mg^{2+} and Ca^{2+} are the most abundant divalent cations in the extracellular fluid. They are essential for the function of many enzymes and for the structure of many biological molecules. They are also involved in the regulation of many physiological processes.

Detailed description of Figure 1: This is a Western blot image showing the expression of p34 and p32 in various tissues. The lanes from left to right are labeled: Kidney, Liver, Spleen, Heart, Lung, Muscle, and Brain. On the right side, molecular weight markers are indicated at 100, 75, 50, and 25 kDa. In the Kidney lane, a strong band for p34 is visible at approximately 34 kDa, and a band for p32 is visible at approximately 32 kDa. In the Liver, Spleen, Heart, Lung, and Muscle lanes, p34 bands are visible at approximately 34 kDa, and p32 bands are visible at approximately 32 kDa. In the Brain lane, a p34 band is visible at approximately 34 kDa, and a p32 band is visible at approximately 32 kDa. The bands for p34 and p32 are indicated by arrows on the right side of the blot.

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XX Therapy. It can also be used to repopulate blood cells in a mammal.
 CC The products can also be used to treat, e.g., reproductive disorders,
 CC arteriosclerosis, Type II diabetes, polycystic ovarian disease,
 CC cardiovascular diseases, osteoarthritis, dermatological disorders,
 CC hypertension, insulin resistance, hypocholsterolemia,
 CC hypertriglyceridemia, cancer and cholestasis.
 XX
 XX Sequence 7127 BP: 1663 A; 1941 G; 1859 G; 1654 T; ...
 Query Match 68.6% Score 19.2; 146 BP; Length 7127
 Best local similarity 87.5% (Prot: No. 91)
 Matches 21: Conservation 91 Mismatches 29 Gaps 12
 4 GTGACCTTACAGACCTTCTCTGAG 26
 ||||| ||||| ||||| |||||
 Tbb 2128 GTGACCTTACAGACCTTCTCTGAG 2151

RESULT 10
 AAT75094
 ID AAT75094 standard: RNA; 7127 BP.
 AC AAT75094;
 XX
 DE 07-021-1997 (first entry)
 XX
 DE Human obesity protein-human 19c1 CH2CH3 gene fusion.
 XX
 KW Obesity protein, Ob protein, 19c1, 111c, 1011c, 111c, 111c,
 KW weight loss; appetite loss; anorexia; polyphagia; hypofunction; OS.
 XX
 OS Chimera Homo sapiens;
 OS Chimera bacteriophage Sp6;
 OS Chimera SV40 virus;
 OS Chimera herpes simplex virus;
 OS Chimera bacteriophage M13.
 XX
 XX Key Location/Qualifiers
 FH 612
 FI misc_RNA
 FI /tag= a
 FI /note= "RNA start"
 FI 776..844
 FI promoter
 FI /tag= b
 FI /note= "Sp6 promoter"
 FI 845
 FI misc_RNA
 FI /tag= c
 FI /note= "Sp6 RNA start"
 FI 918..2112
 FI CDS
 FI /tag= d
 FI 146c1= 08-1991 chimera
 FI 2183
 FI polyA_signal
 FI /tag= e
 FI /note= "SV40 early polyA"
 FI 2124
 FI misc_RNA
 FI /tag= f
 FI /note= "SV40 origin"
 FI 2748
 FI misc_RNA
 FI /tag= g
 FI /note= "pUC118 start"
 FI 2756..2891
 FI promoter
 FI /tag= h
 FI /note= "TK promoter"
 FI 2892..3892
 FI CDS
 FI /tag= i
 FI /note= "TK neomycin phosphotransferase gene"
 FI 3893
 FI terminator
 FI /tag= j
 FI /note= "SV40 late termination"
 FI 4526..4643
 FI misc_RNA
 FI /tag= k
 FI /note= "pBR322 sequence"
 FI 4645
 FI misc_RNA
 FI /tag= l
 FI 1

FI
 XX
 XX Sequence 7127 BP: 1663 A; 1941 G; 1859 G; 1654 T; ...
 Query Match 68.6% Score 19.2; 146 BP; Length 7127
 Best local similarity 87.5% (Prot: No. 91)
 Matches 21: Conservation 91 Mismatches 29 Gaps 12
 4 GTGACCTTACAGACCTTCTCTGAG 26
 ||||| ||||| ||||| |||||
 Tbb 2128 GTGACCTTACAGACCTTCTCTGAG 2151

RESULT 11
 AAT75094
 ID AAT75094 standard: RNA; 7127 BP.
 AC AAT75094;
 XX
 DE 07-021-1997 (first entry)
 XX
 DE Human obesity protein-human 19c1 CH2CH3 gene fusion.
 XX
 KW Obesity protein, Ob protein, 19c1, 111c, 1011c, 111c, 111c,
 KW weight loss; appetite loss; anorexia; polyphagia; hypofunction; OS.
 XX
 OS Chimera Homo sapiens;
 OS Chimera bacteriophage Sp6;
 OS Chimera SV40 virus;
 OS Chimera herpes simplex virus;
 OS Chimera bacteriophage M13.
 XX
 XX Key Location/Qualifiers
 FH 612
 FI misc_RNA
 FI /tag= a
 FI /note= "RNA start"
 FI 776..844
 FI promoter
 FI /tag= b
 FI /note= "Sp6 promoter"
 FI 845
 FI misc_RNA
 FI /tag= c
 FI /note= "Sp6 RNA start"
 FI 918..2112
 FI CDS
 FI /tag= d
 FI 146c1= 08-1991 chimera
 FI 2183
 FI polyA_signal
 FI /tag= e
 FI /note= "SV40 early polyA"
 FI 2124
 FI misc_RNA
 FI /tag= f
 FI /note= "SV40 origin"
 FI 2748
 FI misc_RNA
 FI /tag= g
 FI /note= "pUC118 start"
 FI 2756..2891
 FI promoter
 FI /tag= h
 FI /note= "TK promoter"
 FI 2892..3892
 FI CDS
 FI /tag= i
 FI /note= "TK neomycin phosphotransferase gene"
 FI 3893
 FI terminator
 FI /tag= j
 FI /note= "SV40 late termination"
 FI 4526..4643
 FI misc_RNA
 FI /tag= k
 FI /note= "pBR322 sequence"
 FI 4645
 FI misc_RNA
 FI /tag= l
 FI 1

CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridised to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g., cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations of single nucleotide
 CC polymorphisms (SNPs); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC AB01410-AB054121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.

XX
 SO Sequence 1052 BP: 392 A; 373 C; 143 G; 144 T; 0 other;

Query Match 66.4%; Score 18.6; Len 24; Length 1052;

Best local similarity 84.0%; Pred. No. 1.4e-02;

Matches 21; Conservation 0; Mismatches 4; Indels 0; Gaps 0;

UY 2 CTTCAAGCTTAAAGAGCTTCTCGAG 26

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tb 444 CGGAGAGTTAAAGAGTTATCGAG 420

Search completed: August 14, 2003, 03:52:15
 Job time : 177.491 secs

CC discloses genomic DNA sequences (AB016176-AB016177), expressed RNA
 CC sequences (AB016180-AB016175) and the encoded proteins
 CC (AB016177-AB016172).
 CC The sequence data for this patent did not form part of the prior art
 CC specification, but was obtained in electronic format directly from Wipo
 CC at http://wipo.int/pub/publ/ab016176-177_sequences.
 XX
 XX Sequence 7228 BF: 2135 A; 2447 G; 1507 C; 2135 T; 0 other.
 SU
 Query Match 66.2%; Score 17.2; DB 23; Length 7228
 Best Local Similarity 85.4%; Proc. No. 200027
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0
 YY 1 GATTATGCGTACACTTCG 22
 DB 5436 GCAATACGAGGAGGCTTGG 5415
 RESULT 11
 AB016096/0
 ID AB016096 standard, DNA, 605 bp.
 XX
 AC AB016096;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 2687.
 XX
 KW Human; cytosine methylation; 5'-cpG-3'; orally; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; endocrinological;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 XX
 PN W-200218632 A2.
 XX
 ID 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WC-EP10074.
 XX
 PR 01-SEP-2003; 2003DE 1043826.
 XX
 PR 05-SEP-2000; 2000PF-1044543
 XX
 PA (EP10-) EP10ENOMICS A1.
 XX
 XX
 PI Oldek A, Flapendrock C, Berlin K, Juchacz B.
 XX
 DR WPI: 2002-371929/10.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA; useful
 PT for diagnosis and prognosis; comprises selective hybridization of
 PT amplicons from chemically treated DNA
 XX
 XX Claim 12: 56pp + Sequence Listing: 56pp; German.
 XX
 XX This invention describes a novel method for determining the degree of
 XX methylation of a particular cytosine in a methyl CpG-3' context in a
 XX genomic sample of DNA. The sample is treated chemically to convert
 XX cytosine (C) but not methylated C, to uracil, then part of the genomic
 XX DNA that contains the target C is amplified to form a labeled amplicon.
 XX The amplicon is hybridized to two classes, each with at least one
 XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 XX and the degree of hybridization to both classes is determined from the
 XX label on the amplicon. From the ratio of labels hybridized to the two
 XX classes of oligomers, the degree of methylation is calculated. The method
 XX is used: (i) for diagnosis and/or prognosis of side effects of
 XX therapeutic drugs and of a wide range of diseases, e.g. cancer, fibrosis
 XX of the central nervous, cardiovascular, musculoskeletal and respiratory
 XX systems etc., particularly by detecting mutations of single nucleotide
 XX polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 XX types and for investigating cell differentiation. The method allows the
 XX methylation status of many C residues to be determined simultaneously.

CC Ab016176-AB016177 represent nucleic acid sequences used in accordance with
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.
 XX
 XX Sequence 685 BF: 1000 A; 1000 G; 1000 C; 1000 T; 0 other.
 SU
 Query Match 66.2%; Score 17.2; DB 23; Length 7228
 Best Local Similarity 85.4%; Proc. No. 100027
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0
 YY 2 GATTATGCGTACACTTCG 22
 DB 600 GCAATACGAGGAGGCTTGG 5415
 RESULT 14
 AB016097
 ID AB016097 standard, DNA, 605 bp.
 XX
 AC AB016097;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 2687.
 XX
 KW Human; cytosine methylation; 5'-cpG-3'; orally; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; endocrinological;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 XX
 PN W-200218632 A2.
 XX
 ID 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WC-EP10074.
 XX
 PR 01-SEP-2003; 2003DE 1043826.
 XX
 PR 05-SEP-2000; 2000PF-1044543
 XX
 PA (EP10-) EP10ENOMICS A1.
 XX
 XX
 PI Oldek A, Flapendrock C, Berlin K, Juchacz B.
 XX
 DR WPI: 2002-371929/10.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA; useful
 PT for diagnosis and prognosis; comprises selective hybridization of
 PT amplicons from chemically treated DNA
 XX
 XX Claim 12: 56pp + Sequence Listing: 56pp; German.
 XX
 XX This invention describes a novel method for determining the degree of
 XX methylation of a particular cytosine in a methyl CpG-3' context in a
 XX genomic sample of DNA. The sample is treated chemically to convert
 XX cytosine (C) but not methylated C, to uracil, then part of the genomic
 XX DNA that contains the target C is amplified to form a labeled amplicon.
 XX The amplicon is hybridized to two classes, each with at least one
 XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 XX and the degree of hybridization to both classes is determined from the
 XX label on the amplicon. From the ratio of labels hybridized to the two
 XX classes of oligomers, the degree of methylation is calculated. The method
 XX is used: (i) for diagnosis and/or prognosis of side effects of
 XX therapeutic drugs and of a wide range of diseases, e.g. cancer, fibrosis
 XX of the central nervous, cardiovascular, musculoskeletal and respiratory
 XX systems etc., particularly by detecting mutations of single nucleotide
 XX polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 XX types and for investigating cell differentiation. The method allows the
 XX methylation status of many C residues to be determined simultaneously.
 XX The disclosure of the invention.

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00 discloses genomic DNA sequences (AB016176, AB016177), cDNA and cDNA
01 sequences (AB016180-AB016175) and the encoded proteins
02 (AB027237-AB027202).
03 The sequence data for this patent did not form part of the prior art
04 specification, but was obtained in electronic format directly from WIPO
05 at http://wipo.int/pub/published_pat_sequences.
06
07 Sequence 7228 HF: 2135 A: 1417 C: 1537 G: 2109 T: 6000.
08
09 Query Match 66.28, Score 17.2, E-20, Length 7228
10 Best Local Similarity 86.48, Pctd 82.25, Ids
11 Matches 19, Conservative 0, Mismatches 42, Indels 0, Gaps 0
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00 Abstract: Abstract: Improved genomic DNA sequences used for the detection of
01 method for determining the degree of cytosine methylation. The method
02 for the detection of the human
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04 Sequence 7228 HF: 2135 A: 1417 C: 1537 G: 2109 T: 6000.
05
06 Query Match 66.28, Score 17.2, E-20, Length 7228
07 Best Local Similarity 86.48, Pctd 82.25, Ids
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IBM nucleic - nucleic search, using sw model

Run on: August 14, 2005 ; Search time : 0.00 seconds

₹91.250 Million (₹14,141.250/Share)

Title: US-10-009-962-1

Sequence: 1 CCGTGGAGAACGCTCTTAAAGGTGGATGG 28

Source: Table 1. IDENTITY_NUC

Searchid: 22781392 005, 1215229800 001442

Total number of hits satisfying chosen parameters: 45762784.

Minimum seq length: 0
Maximum seq length: 2000000000

Post-processing: Minimum Match: 0%

List inq first 45 summaries

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1:	em:estba:*
2:	em:esthunn:*
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18:	em:qss:lnv:*
19:	em:qss:pln:*
20:	em:qss:??:*
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23:	em:qss:plv:*
24:	em:qss:plro:*
25:	em:qss:rod:*
26:	em:qss:plnat:*
27:	em:qss:plrl:*
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29:	qb:qss2:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

SUMMARY

Result	Score	Query	Match	Length	pos	th	in set	partition
1	21.2	75.7	555	9	AW72453		AW72453	1
2	20.6	73.6	558	14	U030790		U030790	2
3	20.6	73.6	653	29	B639457		B639457	3
4	20.2	72.1	902	29	U128954		U128954	4

[illegible]

RESULTS

[illegible]

miRNA 506, 100, 110, 133, 145, 155, 192, 200c, 200b, 200a, 200b-1, 200b-2, 200b-3, 200b-4, 200b-5, 200b-6, 200b-7, 200b-8, 200b-9, 200b-10, 200b-11, 200b-12, 200b-13, 200b-14, 200b-15, 200b-16, 200b-17, 200b-18, 200b-19, 200b-20, 200b-21, 200b-22, 200b-23, 200b-24, 200b-25, 200b-26, 200b-27, 200b-28, 200b-29, 200b-30, 200b-31, 200b-32, 200b-33, 200b-34, 200b-35, 200b-36, 200b-37, 200b-38, 200b-39, 200b-40, 200b-41, 200b-42, 200b-43, 200b-44, 200b-45, 200b-46, 200b-47, 200b-48, 200b-49, 200b-50, 200b-51, 200b-52, 200b-53, 200b-54, 200b-55, 200b-56, 200b-57, 200b-58, 200b-59, 200b-60, 200b-61, 200b-62, 200b-63, 200b-64, 200b-65, 200b-66, 200b-67, 200b-68, 200b-69, 200b-70, 200b-71, 200b-72, 200b-73, 200b-74, 200b-75, 200b-76, 200b-77, 200b-78, 200b-79, 200b-80, 200b-81, 200b-82, 200b-83, 200b-84, 200b-85, 200b-86, 200b-87, 200b-88, 200b-89, 200b-90, 200b-91, 200b-92, 200b-93, 200b-94, 200b-95, 200b-96, 200b-97, 200b-98, 200b-99, 200b-100, 200b-101, 200b-102, 200b-103, 200b-104, 200b-105, 200b-106, 200b-107, 200b-108, 200b-109, 200b-110, 200b-111, 200b-112, 200b-113, 200b-114, 200b-115, 200b-116, 200b-117, 200b-118, 200b-119, 200b-120, 200b-121, 200b-122, 200b-123, 200b-124, 200b-125, 200b-126, 200b-127, 200b-128, 200b-129, 200b-130, 200b-131, 200b-132, 200b-133, 200b-134, 200b-135, 200b-136, 200b-137, 200b-138, 200b-139, 200b-140, 200b-141, 200b-142, 200b-143, 200b-144, 200b-145, 200b-146, 200b-147, 200b-148, 200b-149, 200b-150, 200b-151, 200b-152, 200b-153, 200b-154, 200b-155, 200b-156, 200b-157, 200b-158, 200b-159, 200b-160, 200b-161, 200b-162, 200b-163, 200b-164, 200b-165, 200b-166, 200b-167, 200b-168, 200b-169, 200b-170, 200b-171, 200b-172, 200b-173, 200b-174, 200b-175, 200b-176, 200b-177, 200b-178, 200b-179, 200b-180, 200b-181, 200b-182, 200b-183, 200b-184, 200b-185, 200b-186, 200b-187, 200b-188, 200b-189, 200b-190, 200b-191, 200b-192, 200b-193, 200b-194, 200b-195, 200b-196, 200b-197, 200b-198, 200b-199, 200b-200, 200b-201, 200b-202, 200b-203, 200b-204, 200b-205, 200b-206, 200b-207, 200b-208, 200b-209, 200b-210, 200b-211, 200b-212, 200b-213, 200b-214, 200b-215, 200b-216, 200b-217, 200b-218, 200b-219, 200b-220, 200b-221, 200b-222, 200b-223, 200b-224, 200b-225, 200b-226, 200b-227, 200b-228, 200b-229, 200b-230, 200b-231, 200b-232, 200b-233, 200b-234, 200b-235, 200b-236, 200b-237, 200b-238, 200b-239, 200b-240, 200b-241, 200b-242, 200b-243, 200b-244, 200b-245, 200b-246, 200b-247, 200b-248, 200b-249, 200b-250, 200b-251, 200b-252, 200b-253, 200b-254, 200b-255, 200b-256, 200b-257, 200b-258, 200b-259, 200b-260, 200b-261, 200b-262, 200b-263, 200b-264, 200b-265, 200b-266, 200b-267, 200b-268, 200b-269, 200b-270, 200b-271, 200b-272, 200b-273, 200b-274, 200b-275, 200b-276, 200b-277, 200b-278, 200b-279, 200b-280, 200b-281, 200b-282, 200b-283, 200b-284, 200b-285, 200b-286, 200b-287, 200b-288, 200b-289, 200b-290, 200b-291, 200b-292, 200b-293, 200b-294, 200b-295, 200b-296, 200b-297, 200b-298, 200b-299, 200b-300, 200b-301, 200b-302, 200b-303, 200b-304, 200b-305, 200b-306, 200b-307, 200b-308, 200b-309, 200b-310, 200b-311, 200b-312, 200b-313, 200b-314, 200b-315, 200b-316, 200b-317, 200b-318, 200b-319, 200b-320, 200b-321, 200b-322, 200b-323, 200b-324, 200b-325, 200b-326, 200b-327, 200b-328, 200b-329, 200b-330, 200b-331, 200b-332, 200b-333, 200b-334, 200b-335, 200b-336, 200b-337, 200b-338, 200b-339, 200b-340, 200b-341, 200b-342, 200b-343, 200b-344, 200b-345, 200b-346, 200b-347, 200b-348, 200b-349, 200b-350, 200b-351, 200b-352, 200b-353, 200b-354, 200b-355, 200b-356, 200b-357, 200b-358, 200b-359, 200b-360, 200b-361, 200b-362, 200b-363, 200b-364, 200b-365, 200b-366, 200b-367, 200b-368, 200b-369, 200b-370, 200b-371, 200b-372, 200b-373, 200b-374, 200b-375, 200b-376, 200b-377, 200b-378, 200b-379, 200b-380, 200b-381, 200b-382, 200b-383, 200b-384, 200b-385, 200b-386, 200b-387, 200b-388, 200b-389, 200b-390, 200b-391, 200b-392, 200b-393, 200b-394, 200b-395, 200b-396, 200b-397, 200b-398, 200b-399, 200b-400, 200b-401, 200b-402, 200b-403, 200b-404, 200b-405, 200b-406, 200b-407, 200b-408, 200b-409, 200b-410, 200b-411, 200b-412, 200b-413, 200b-414, 200b-4

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For the purpose of this study, the following compounds were selected: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838

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GenCore version 5.1.4
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2003, 02:24:05, Search time 17.06 seconds
(without alignment) 391.190 Million cell updates/sec

Title: US-10-009-962-2
Perfect score: 28
Sequence: 1 CCGTGGACCTTAGAGCTTTCGAG36 28

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 15562764

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: EST:
1: em_estba:
2: em_estbun:
3: em_estin:
4: em_estmu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_hic:
9: qb_est1:
10: qb_est2:
11: qb_hic:
12: qb_est3:
13: qb_est4:
14: qb_est5:
15: em_estom:
16: em_estom:
17: em_gss_hum:
18: em_gss_hum:
19: em_gss_hum:
20: em_gss_vrl:
21: em_gss_fun:
22: em_gss_mam:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_pro:
26: em_gss_pro:
27: em_gss_vrl:
28: qb_gss1:
29: qb_gss2:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	FW	ID	Description
1	21.2	75.7	555	9	AW577491	AW577491.1 (1866 bp)
2	20.6	73.6	553	14	AW577491	AW577491.2 (1866 bp)
3	20.6	73.6	553	29	B2439457	B2439457.B01211K
4	20.2	72.1	903	26	CC424864	CC424864.F000047K

Result	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
1	AW577491	EST	AW577491	1	EST	Shimokawa, K. (2003)	Shimokawa, K. (2003)
2	AW577491	EST	AW577491	2	EST	Shimokawa, K. (2003)	Shimokawa, K. (2003)
3	B2439457	B01211K	B2439457	1	B01211K	Shimokawa, K. (2003)	Shimokawa, K. (2003)
4	CC424864	F000047K	CC424864	1	F000047K	Shimokawa, K. (2003)	Shimokawa, K. (2003)

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AUTHORS
TITLE
JOURNAL
GENEID
WU
Washington University School of Medicine

/clone="H101"
 /note="Vector: PHOS1; Size: 1.6 kb sheared
 total DNA inserted into phos1 using BstXI linker"

BASE COUNT 178 a 137 c 192 g 145 t
 ORIGIN

Query Match 73.6% Score 20.6; Pos 29; Length 656
 Best Local Similarity 85.2% Pos 60; Length 656
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0

RESULT 4
 CC424864 803 bp DNA Linear Nov 19 MAY 2003
 DEFINITION genomic survey sequence.
 VERSION CC424864.1 GI:30904954
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 1 (bases 1 to 803)
 AUTHORS White, C. A., Quisenberry, T., Van Auken, M., et al. 1997.
 A. Fraser, C.M., Yuan, Y., San Miguel, P., Majd, and International
 Maize Genomics Consortium
 JOURNAL Unpublished
 COMMENT Contact: Cathy Whitelaw
 TIGR 9712 Medical Center, Chevy Chase, MD 20815, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: T6
 class: sheared ends.
 Location/Qualifiers
 1..803

/organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="H73"
 /db_xref="taxon:100647200"
 /clone="ZM_0.6_1.0_KB"
 /note="Vector: PCR TOPO; Size: 0.6-1.0 kb high
 cot selected genomic DNA library"
 BASE COUNT 244 a 162 c 161 g 236 t
 ORIGIN

Query Match 72.1% Score 20.2; Pos 29; Length 656
 Best Local Similarity 88.0% Pos 60; Length 656
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0

RESULT 5
 B0102444 504 bp mRNA Linear EST screened by
 Locus B0102444
 DEFINITION 109101B01.X1 1091; immature leaf with common ESTs screened by
 B0102444
 ACCESSION B0102444
 VERSION B0102444.1 GI:22552405
 KEYWORDS EST.
 SOURCE Zea mays

/organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="taxon:100647200"
 /clone="ZM_0.6_1.0_KB"
 /note="Vector: PCR TOPO; Size: 0.6-1.0 kb high
 cot selected genomic DNA library"
 BASE COUNT 244 a 162 c 161 g 236 t
 ORIGIN

/organism="Zea mays"
 /note="Vector: PHOS1; Size: 1.6 kb sheared
 total DNA inserted into phos1 using BstXI linker"

BASE COUNT 178 a 137 c 192 g 145 t
 ORIGIN

Query Match 73.6% Score 20.6; Pos 29; Length 656
 Best Local Similarity 85.2% Pos 60; Length 656
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0

RESULT 4
 CC424864 803 bp DNA Linear Nov 19 MAY 2003
 DEFINITION genomic survey sequence.
 VERSION CC424864.1 GI:30904954
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

/organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="H73"
 /db_xref="taxon:100647200"
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 /note="Vector: PCR TOPO; Size: 0.6-1.0 kb high
 cot selected genomic DNA library"
 BASE COUNT 244 a 162 c 161 g 236 t
 ORIGIN

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 Best Local Similarity 88.0% Pos 60; Length 656
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 Locus B0102444
 DEFINITION 109101B01.X1 1091; immature leaf with common ESTs screened by
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 ACCESSION B0102444
 VERSION B0102444.1 GI:22552405
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

/organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="taxon:100647200"
 /clone="ZM_0.6_1.0_KB"
 /note="Vector: PCR TOPO; Size: 0.6-1.0 kb high
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 BASE COUNT 244 a 162 c 161 g 236 t
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/organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="taxon:100647200"
 /clone="ZM_0.6_1.0_KB"
 /note="Vector: PCR TOPO; Size: 0.6-1.0 kb high
 cot selected genomic DNA library"
 BASE COUNT 244 a 162 c 161 g 236 t
 ORIGIN



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0.5

1. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx$
 2. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx$
 3. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx$
 4. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx$
 5. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx$
 6. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx$
 7. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx$
 8. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx$
 9. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx$
 10. $\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \int_{\mathbb{R}^n} u \Delta u dx$

1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

```

graph TD
    A[Selection of a sample of 1000 subjects] --> B[Random assignment to two groups]
    B --> C[Control]
    B --> D[Intervention]
    C --> E[No intervention]
    D --> F[Intervention]
    E --> G[Follow-up for 12 months]
    F --> G
    G --> H[Health status]
  
```

1. *Phragmites australis* (Cav.) Trin. ex Steud.

[illegible]

Figure 1 shows a Western blot analysis of p38 phosphorylation. The blot is divided into two main sections: 'p-p38' (phosphorylated p38) and 'p38' (total p38). The lanes represent different cell lines and treatments: MDA-MB-231, MCF-7, T47D, BT20, ZR75.1, BT20, ZR75.1, BT20, ZR75.1. The treatments are Control, IL-1, IL-1 + SB, and IL-1 + SB + JNK inhibitor. Molecular weight markers are indicated on the right side of the blot.

[illegible]

Mathematics 2022, 10, 1111

[illegible][illegible][illegible]

Michigan, A.

100

As a result of the above, the following theorem can be proved.

100

[illegible]

Figure 1

[illegible]

1. *Chlorophyll a* (Chl *a*)
 2. *Chlorophyll b* (Chl *b*)
 3. *Chlorophyll c* (Chl *c*)
 4. *Chlorophyll d* (Chl *d*)
 5. *Chlorophyll e* (Chl *e*)
 6. *Chlorophyll f* (Chl *f*)
 7. *Chlorophyll g* (Chl *g*)
 8. *Chlorophyll h* (Chl *h*)
 9. *Chlorophyll i* (Chl *i*)
 10. *Chlorophyll j* (Chl *j*)
 11. *Chlorophyll k* (Chl *k*)
 12. *Chlorophyll l* (Chl *l*)
 13. *Chlorophyll m* (Chl *m*)
 14. *Chlorophyll n* (Chl *n*)
 15. *Chlorophyll o* (Chl *o*)
 16. *Chlorophyll p* (Chl *p*)
 17. *Chlorophyll q* (Chl *q*)
 18. *Chlorophyll r* (Chl *r*)
 19. *Chlorophyll s* (Chl *s*)
 20. *Chlorophyll t* (Chl *t*)
 21. *Chlorophyll u* (Chl *u*)
 22. *Chlorophyll v* (Chl *v*)
 23. *Chlorophyll w* (Chl *w*)
 24. *Chlorophyll x* (Chl *x*)
 25. *Chlorophyll y* (Chl *y*)
 26. *Chlorophyll z* (Chl *z*)
 27. *Chlorophyll aa* (Chl *aa*)
 28. *Chlorophyll ab* (Chl *ab*)
 29. *Chlorophyll ac* (Chl *ac*)
 30. *Chlorophyll ad* (Chl *ad*)
 31. *Chlorophyll ae* (Chl *ae*)
 32. *Chlorophyll af* (Chl *af*)
 33. *Chlorophyll ag* (Chl *ag*)
 34. *Chlorophyll ah* (Chl *ah*)
 35. *Chlorophyll ai* (Chl *ai*)
 36. *Chlorophyll aj* (Chl *aj*)
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 38. *Chlorophyll al* (Chl *al*)
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 40. *Chlorophyll an* (Chl *an*)
 41. *Chlorophyll ao* (Chl *ao*)
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 44. *Chlorophyll ar* (Chl *ar*)
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 55. *Chlorophyll acz* (Chl *acz*)
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 58. *Chlorophyll afz* (Chl *afz*)
 59. *Chlorophyll agz* (Chl *agz*)
 60. *Chlorophyll ahz* (Chl *ahz*)
 61. *Chlorophyll aiz* (Chl *aiz*)
 62. *Chlorophyll ajz* (Chl *ajz*)
 63. *Chlorophyll akz* (Chl *akz*)
 64. *Chlorophyll alz* (Chl *alz*)
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 100. *Chlorophyll auz* (Chl *auz*)
 101. *Chlorophyll avz* (Chl *avz*)
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 132. *Chlorophyll ayz* (Chl *ayz*)
 133.

[illegible]

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100

[illegible]
$$\frac{1}{V} \frac{dV}{dt} = \frac{1}{V} \frac{dV}{d\lambda} \frac{d\lambda}{dt}$$
$$H^1(\mathbb{R}^n, \mathbb{R}) \cong \mathbb{R}^n$$

cy 1 GCATTAAACAGCTAGCACTTC 21
 || ||||||| ||
fb 112 GCTTAATCAGCTAGCACTTC 92

KF:SUJL 15
A1657536

LOCUS	583 bp	mRNA	1100 nt	1995 MAY 1995
DEFINITION	Aedes aegypti MT pSPART library	Aedes aegypti cDNA clone		
ACCESSION	AF165753			

ACCESSION	AI657536
REVISION	AI657536-1
STATION	ST-47E3600

KEYWORDS **LIST**
SUBJECT **Address**

ECUANISM
Aedes aegypti
Eubacterium motacris

REFERENCE 1 (bases 1 to 583)

TITLE Expressed sequence tags of cDNA clones from an enriched polyploidar tubule and out tubule from *Boea matronalis*

COMMENT
Contact: GILL SS
Phone: 415 435 1111

5419 Boyce Hall, Riverside, CA 92521, USA

Email: sarjeet.gill@nrc.ca

REFERENCES

/organism "envy" /mol_type "mRNA"

$$/ \text{SCX} = \text{t emal } c^n$$

```
/dev_stage "adulc"
/lab_host "PH103"
```

Whole vector, properly site-1:

CONCLUSION

	Best Local Similarity	90.58;	Pred. No.	1.40004;
Matches	19; Conservative	0;	Mismatches	7;

5 ATTCAGCTAGCACTTCGATACG 26

.job time : 1624.87 secs

Downloaded from <http://ajph.org/> on November 10, 2014

Query Match:	68.5%;	Score 17.8;	Pr: 9;	Length 583;
Host Local Similarity	90.5%;	Pred. No. 1.40e04;		
Matches 19;	Conservative	0;	Mismatches 2;	Indels 0;
			Gaps	0

5 AATCAGCTACCACTTCGACG 26

529 AATTAGCTAACACCTTGATTC 549

Search completed: August 14, 2003, 05:46:44

Search completed: August 14, 2008, 05:46:44
Job time : 1624.87 secs

Job time : 16.24.87 sec's

1
2
3

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Molecule - nucleotide search, using sw model

Run on: August 14, 2003, 02:24:05 ; Search time 10.15.47 Seconds
(without alignments) 391.190 Million cels: updates/sec

Title: US-10-009-962-4

Perfect score: 26
Sequence: 1 CGTGGACAGCTGCAATGATATATAGC 26

Scoring table: IDENTITY_N9C
Gapop 10.0 / Gapext 1.0

Searched: 22791392 seqs, 1217239056, 8021360

Total number of hits satisfying chosen parameters: 4562794

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 9%

Listing first 45 summaries

Database :

EST*
1: em_estba:*
2: em_esthu:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: qb_est1:*
10: qb_est2:*
11: qb_hlc:*
12: qb_est3:*
13: qb_est4:*
14: qb_est5:*
15: em_esthu:*
16: em_estro:*
17: em_qss_hum:*
18: em_qss_hu:*
19: em_qss_pla:*
20: em_qss_vet:*
21: em_qss_fun:*
22: em_qss_mam:*
23: em_qss_mus:*
24: em_qss_pra:*
25: em_qss_ror:*
26: em_qss_pha:*
27: em_qss_vr1:*
28: qb_qss1:*
29: qb_qss2:*

Prod. No. is the number of results produced by engine to have a score greater than or equal to the score of the result below. Prod. No. is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query Match	Length	Prod. No.	Accession
1	18.8	72.3	509	28	A2928060
2	18.8	72.3	645	29	B2405494
3	18.8	72.3	680	29	B2405505
4	18.6	71.5	181	9	AA514111

5	18.6	71.5	600	12	B6117962
6	18.6	71.5	115	12	B6100142
7	18.6	71.5	600	12	AA145539
8	18.6	71.5	600	12	B6117962
9	18.6	71.5	600	12	AA145539
10	18.6	71.5	600	12	AA145539
11	18.6	71.5	600	12	AA145539
12	18.6	71.5	600	12	AA145539
13	18.6	71.5	600	12	AA145539
14	18.6	71.5	600	12	AA145539
15	18.6	71.5	600	12	AA145539
16	18.6	71.5	600	12	AA145539
17	18.6	71.5	600	12	AA145539
18	18.6	71.5	600	12	AA145539
19	18.6	71.5	600	12	AA145539
20	18.6	71.5	600	12	AA145539
21	18.6	71.5	600	12	AA145539
22	18.6	71.5	600	12	AA145539
23	18.6	71.5	600	12	AA145539
24	18.6	71.5	600	12	AA145539
25	18.6	71.5	600	12	AA145539
26	18.6	71.5	600	12	AA145539
27	18.6	71.5	600	12	AA145539
28	18.6	71.5	600	12	AA145539
29	18.6	71.5	600	12	AA145539
30	18.6	71.5	600	12	AA145539
31	18.6	71.5	600	12	AA145539
32	18.6	71.5	600	12	AA145539
33	18.6	71.5	600	12	AA145539
34	18.6	71.5	600	12	AA145539
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37	18.6	71.5	600	12	AA145539
38	18.6	71.5	600	12	AA145539
39	18.6	71.5	600	12	AA145539
40	18.6	71.5	600	12	AA145539
41	18.6	71.5	600	12	AA145539
42	18.6	71.5	600	12	AA145539
43	18.6	71.5	600	12	AA145539
44	18.6	71.5	600	12	AA145539
45	18.6	71.5	600	12	AA145539

ADDITIONS:

RESULT 1
Accession: A2928060
Definition: 179,411 nt cDNA sequence from human skin fibroblasts
Accession: A2928060
Keywords: EST, cDNA, Human, Skin, Fibroblasts
Source: GenBank
Organism: Homo sapiens
Reference: 1. Human Genome Project, Nature 391:31-34 (1998)
2. Human Genome Project, Nature 391:31-34 (1998)
3. Human Genome Project, Nature 391:31-34 (1998)
4. Human Genome Project, Nature 391:31-34 (1998)
5. Human Genome Project, Nature 391:31-34 (1998)
6. Human Genome Project, Nature 391:31-34 (1998)
7. Human Genome Project, Nature 391:31-34 (1998)
8. Human Genome Project, Nature 391:31-34 (1998)
9. Human Genome Project, Nature 391:31-34 (1998)
10. Human Genome Project, Nature 391:31-34 (1998)
11. Human Genome Project, Nature 391:31-34 (1998)
12. Human Genome Project, Nature 391:31-34 (1998)
13. Human Genome Project, Nature 391:31-34 (1998)
14. Human Genome Project, Nature 391:31-34 (1998)
15. Human Genome Project, Nature 391:31-34 (1998)
16. Human Genome Project, Nature 391:31-34 (1998)
17. Human Genome Project, Nature 391:31-34 (1998)
18. Human Genome Project, Nature 391:31-34 (1998)
19. Human Genome Project, Nature 391:31-34 (1998)
20. Human Genome Project, Nature 391:31-34 (1998)
21. Human Genome Project, Nature 391:31-34 (1998)
22. Human Genome Project, Nature 391:31-34 (1998)
23. Human Genome Project, Nature 391:31-34 (1998)
24. Human Genome Project, Nature 391:31-34 (1998)
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31. Human Genome Project, Nature 391:31-34 (1998)
32. Human Genome Project, Nature 391:31-34 (1998)
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34. Human Genome Project, Nature 391:31-34 (1998)
35. Human Genome Project, Nature 391:31-34 (1998)
36. Human Genome Project, Nature 391:31-34 (1998)
37. Human Genome Project, Nature 391:31-34 (1998)
38. Human Genome Project, Nature 391:31-34 (1998)
39. Human Genome Project, Nature 391:31-34 (1998)
40. Human Genome Project, Nature 391:31-34 (1998)
41. Human Genome Project, Nature 391:31-34 (1998)
42. Human Genome Project, Nature 391:31-34 (1998)
43. Human Genome Project, Nature 391:31-34 (1998)
44. Human Genome Project, Nature 391:31-34 (1998)
45. Human Genome Project, Nature 391:31-34 (1998)

SOURCE

1. JRL
 /organism "Schistosoma mansoni"
 /mol_type "mRNA"
 /db_xref "taxon:5183"
 /clone "AS-17"
 /sex "mixed"
 /dev_stage "adult"
 /clone_lib "S. mansoni adult lambda Zap"
 /note "Library provided by Dr. M. Salter JRL, Cairo, Egypt"

BASE COUNT 49 a 33 c 33 g 66 t

ORIGIN

Query Match 71.5% Score 18.6; EMB 3; Length 101
 Best Local Similarity 84.0% EMB No. 476022
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0

1 CCGTGAAGTGGTCACTGATTAATG 25
 ||||| ||||| ||||| ||||| |||||
 40 GCTTAAGTGGTCACTGATTAATG 64

RESULT 5
 BM447991/6
 LOCUS 460 bp mRNA linear EST of A066475
 DEFINITION D5A021807.5663 An expressed sequence tag database for the halotolerant green alga Dunaliella salina Dunaliella salina strain 5663 clone D5A021807.5, mRNA sequence.

ACCESSION
 VERSION BM447991.1 GI:19854563
 KEYWORDS
 SOURCE Dunaliella salina
 ORGANISM Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Dunaliellaceae; Dunaliella

REFERENCE
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the halotolerant green alga Dunaliella salina
 JOURNAL Unpublished
 CONTACT: Cushman, J.C.
 Department of Biochemistry
 University of Nevada
 MS209, Reno, NV 89567-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu

PCR Primers
 FORWARD: T4 20mer
 BACKWARD: T7 21mer
 Plate: 021 row: B column: 07
 Seq primer: T4 20mer
 High quality sequencer stop: 360.
 Location/Qualifiers

FEATURES
 Source

1..360
 /organism "Dunaliella salina"
 /mol_type "mRNA"
 /db_xref "taxon:3046"
 /clone "D5A021807"
 /tissue_type "cells, which was adapted to 2.5 M NaCl and a incremental series from 1.7 to 2.0 to 2.5 to 2.5 M NaCl, were exposed to 3.4 M NaCl for 5 hours"
 /cell_type "green"

1. 360
 /organism "Dunaliella salina"
 /mol_type "mRNA"
 /db_xref "taxon:3046"
 /clone "D5A021807"
 /tissue_type "cells, which was adapted to 2.5 M NaCl and a incremental series from 1.7 to 2.0 to 2.5 to 2.5 M NaCl, were exposed to 3.4 M NaCl for 5 hours"
 /cell_type "green"

BASE COUNT 95 a 76 c 131 g 58 t

ORIGIN

Query Match 71.5% Score 18.6; EMB 3; Length 101

Best Local Similarity 84.0% EMB No. 476022
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0

1 CCGTGAAGTGGTCACTGATTAATG 25
 ||||| ||||| ||||| ||||| |||||
 40 GCTTAAGTGGTCACTGATTAATG 64

RESULT 6
 BM447991/6
 LOCUS 460 bp mRNA linear EST of A066475
 DEFINITION D5A021807.5663 An expressed sequence tag database for the halotolerant green alga Dunaliella salina Dunaliella salina strain 5663 clone D5A021807.5, mRNA sequence.

ACCESSION
 VERSION BM447991.1 GI:19854563
 KEYWORDS
 SOURCE Dunaliella salina
 ORGANISM Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Dunaliellaceae; Dunaliella

REFERENCE
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the halotolerant green alga Dunaliella salina
 JOURNAL Unpublished
 CONTACT: Cushman, J.C.
 Department of Biochemistry
 University of Nevada
 MS209, Reno, NV 89567-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu

PCR Primers
 FORWARD: T4 20mer
 BACKWARD: T7 21mer
 Plate: 021 row: B column: 07
 Seq primer: T4 20mer
 High quality sequencer stop: 360.
 Location/Qualifiers

FEATURES
 Source

1..360
 /organism "Dunaliella salina"
 /mol_type "mRNA"
 /db_xref "taxon:3046"
 /clone "D5A021807"
 /tissue_type "cells, which was adapted to 2.5 M NaCl and a incremental series from 1.7 to 2.0 to 2.5 to 2.5 M NaCl, were exposed to 3.4 M NaCl for 5 hours"
 /cell_type "green"

1. 360
 /organism "Dunaliella salina"
 /mol_type "mRNA"
 /db_xref "taxon:3046"
 /clone "D5A021807"
 /tissue_type "cells, which was adapted to 2.5 M NaCl and a incremental series from 1.7 to 2.0 to 2.5 to 2.5 M NaCl, were exposed to 3.4 M NaCl for 5 hours"
 /cell_type "green"

BASE COUNT 95 a 76 c 131 g 58 t

ORIGIN

Query Match 71.5% Score 18.6; EMB 3; Length 101
 Best Local Similarity 84.0% EMB No. 476022
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0

1 CCGTGAAGTGGTCACTGATTAATG 25
 ||||| ||||| ||||| ||||| |||||
 40 GCTTAAGTGGTCACTGATTAATG 64

RESULT 7
 BM447991/6
 LOCUS 460 bp mRNA linear EST of A066475
 DEFINITION D5A021807.5663 An expressed sequence tag database for the halotolerant green alga Dunaliella salina Dunaliella salina strain 5663 clone D5A021807.5, mRNA sequence.

ACCESSION
 VERSION BM447991.1 GI:19854563
 KEYWORDS
 SOURCE Dunaliella salina
 ORGANISM Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Dunaliellaceae; Dunaliella

REFERENCE
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the halotolerant green alga Dunaliella salina
 JOURNAL Unpublished
 CONTACT: Cushman, J.C.
 Department of Biochemistry
 University of Nevada
 MS209, Reno, NV 89567-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu

DATE: 08/14/03 09:09:41 2003

TO: DIRECTOR, FBI
FROM: SAC, NEW YORK (100-100000)
SUBJECT: [REDACTED]

1. [REDACTED]

2. [REDACTED]

3. [REDACTED]

4. [REDACTED]

5. [REDACTED]

6. [REDACTED]

7. [REDACTED]

8. [REDACTED]

9. [REDACTED]

10. [REDACTED]

11. [REDACTED]

12. [REDACTED]

13. [REDACTED]

14. [REDACTED]

15. [REDACTED]

16. [REDACTED]

17. [REDACTED]

18. [REDACTED]

19. [REDACTED]

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22. [REDACTED]

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25. [REDACTED]

26. [REDACTED]

27. [REDACTED]

28. [REDACTED]

29. [REDACTED]

30. [REDACTED]

31. [REDACTED]

32. [REDACTED]

33. [REDACTED]

34. [REDACTED]

35. [REDACTED]

36. [REDACTED]

37. [REDACTED]

38. [REDACTED]

39. [REDACTED]

40. [REDACTED]

41. [REDACTED]

42. [REDACTED]

43. [REDACTED]

44. [REDACTED]

45. [REDACTED]

46. [REDACTED]

47. [REDACTED]

48. [REDACTED]

49. [REDACTED]

5 GAAGTCTAGCTGATTGATCT 26
 1111111111111111111111
 92 GAAGTCTAGCTGATTGATCT 112

RESULT 15

AL657536/

AL657536 mRNA 584 bp. EST 05-MAY 1997

DEFINITION: Aedes aegypti: mRNA sequence.

AL657536

AL657536.1 GI:4753526

EST. Aedes aegypti (yellow fever mosquito)

ORGANISM: Aedes aegypti (yellow fever mosquito)

REFERENCE: Eukaryota: Metazoa: Arthropoda: Insecta: Phlebotominae: Neoptera: Endopterygota: Diptera: Nematocera: Culicidae: Aedes.

1 (bases 1 to 583)

Gill, S. S., Ross, L. S., and Madlak, R. Expressed sequence tags of cDNA clones from an enriched Malpighian tubule and gut library from Aedes aegypti

Unpublished

CONTACT: Gill, S.S.

Environmental Toxicology

University of California, Riverside

5419 Boyce Hall, Riverside, CA 92521, USA

tel: 909 787 3547

Fax: 909 787 3087

Email: sarjeet.gill@ucr.edu

Seq primer: CCAGTCTCTAATGCACTGACAT

High quality sequence stop: 583.

Location/Qualifiers

1..583

/organism "Aedes aegypti"

/mol_type "mRNA"

/db_xref "taxon:7159"

/cdate "05/97"

/sex "female"

/tissue_type "malpighian tubules and gut"

/dev_stage "adult"

/lab_host "MH108"

/cdate "11/97" Aedes aegypti M1 (Shope Library)

Note "Vector: pSP6B1; Site: SalI; Site: NotI; The cDNA was cloned into the SalI/NotI sites of pSP6B1."

BASE COUNT 162 a 130 c 143 g 146 t

ORIGIN

Query Match 68.58; Score 17.8; DB 9; Length 584;

Best local Similarity 90.58; Fred. No. 1.4e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 GTCGCACTGCTGATTGAT 21

1111111111111111111111

DB 549 GATGCACTGATTGATT 529

Search completed: August 14, 2003, 09:46:45

Job time: 1617.87 secs



Query Match: 65.7%; Score 18.4; DB 4; Length 1416
 Best Local Similarity: 78.6%; Prod. No. 24
 Matches: 22; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0

Q7 1 CCGTCAACGCTCTTACGTCACG 28
 111111111111111111111111
 DB 116 CCGTCAACGCTCTTACGTCACG 44

RESULT 6
 US-09-252-991A-1512
 ? Sequence 1512, Application US/09-252-991A
 ? Patent No. 6551795
 ? GENERAL INFORMATION:
 ? APPLICANT: Marc J. Rubinfeld et al.
 ? TITLE OF INVENTION: SUGGESTION FOR AN AMINO ACID-CONTAINING SEQUENTIAL POLYMER
 ? FILE REFERENCE: 107196.136
 ? CURRENT FILING DATE: 1999-02-18
 ? PRIOR FILING DATE: 1998-02-18
 ? PRIOR APPLICATION NUMBER: US 60/094,198
 ? PRIOR FILING DATE: 1998-07-27
 ? NUMBER OF SEQ ID NOS: 34142
 ? SEQ ID NO: 1512
 ? LENGTH: 1416
 ? TYPE: LNA
 ? ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-1512

Query Match: 65.7%; Score 18.4; DB 4; Length 1416
 Best Local Similarity: 78.6%; Prod. No. 24
 Matches: 22; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0

Q7 1 CCGTCAACGCTCTTACGTCACG 28
 111111111111111111111111
 DB 878 CCGTCAACGCTCTTACGTCACG 951

RESULT 7
 US-09-252-991A-1464
 ? Sequence 1464, Application US/09-252-991A
 ? Patent No. 6551795
 ? GENERAL INFORMATION:
 ? APPLICANT: Marc J. Rubinfeld et al.
 ? TITLE OF INVENTION: SUGGESTION FOR AN AMINO ACID-CONTAINING SEQUENTIAL POLYMER
 ? FILE REFERENCE: 107196.136
 ? CURRENT FILING DATE: 1999-02-18
 ? PRIOR FILING DATE: 1998-02-18
 ? PRIOR APPLICATION NUMBER: US 60/094,198
 ? PRIOR FILING DATE: 1998-07-27
 ? NUMBER OF SEQ ID NOS: 34142
 ? SEQ ID NO: 1464
 ? LENGTH: 2352
 ? TYPE: LNA
 ? ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-1464

Query Match: 65.7%; Score 18.4; DB 4; Length 1416
 Best Local Similarity: 78.6%; Prod. No. 24
 Matches: 22; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0

Q7 1 CCGTCAACGCTCTTACGTCACG 28
 111111111111111111111111
 DB 44 CCGTCAACGCTCTTACGTCACG 807

RESULT 8
 US-09-252-991A-1563

Query Match: 65.7%; Score 18.4; DB 4; Length 1416
 Best Local Similarity: 78.6%; Prod. No. 24
 Matches: 22; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0

Q7 1 CCGTCAACGCTCTTACGTCACG 28
 111111111111111111111111
 DB 116 CCGTCAACGCTCTTACGTCACG 44

RESULT 9
 US-09-105-483-211
 ? Sequence 211, Application US/09-105-483
 ? Patent No. 6498407
 ? GENERAL INFORMATION:
 ? APPLICANT: Marc J. Rubinfeld et al.
 ? TITLE OF INVENTION: SUGGESTION FOR AN AMINO ACID-CONTAINING SEQUENTIAL POLYMER
 ? FILE REFERENCE: 107196.136
 ? CURRENT FILING DATE: 1999-02-18
 ? PRIOR FILING DATE: 1998-02-18
 ? PRIOR APPLICATION NUMBER: US 60/094,198
 ? PRIOR FILING DATE: 1998-07-27
 ? NUMBER OF SEQ ID NOS: 34142
 ? SEQ ID NO: 211
 ? LENGTH: 1416
 ? TYPE: LNA
 ? ORGANISM: Pseudomonas aeruginosa
 US-09-105-483-211

NAME: MATH
 ADDRESS: 201 10th St, N, Apt 10, Minneapolis, MN 55401
 CITY: MINNEAPOLIS, STATE: MN, COUNTRY: USA
 PHONE: 612 338 1234

PERSONAL

NAME: MATH

ADDRESS: 201 10th St, N, Apt 10, Minneapolis, MN 55401

CITY: MINNEAPOLIS, STATE: MN, COUNTRY: USA

PHONE: 612 338 1234

NAME: MATH

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NAME: MATH

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CITY: MINNEAPOLIS, STATE: MN, COUNTRY: USA

PHONE: 612 338 1234

NAME: MATH

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CITY: MINNEAPOLIS, STATE: MN, COUNTRY: USA

PHONE: 612 338 1234

NAME: MATH

ADDRESS: 201 10th St, N, Apt 10, Minneapolis, MN 55401

CITY: MINNEAPOLIS, STATE: MN, COUNTRY: USA

PHONE: 612 338 1234

NAME: MATH

ADDRESS: 201 10th St, N, Apt 10, Minneapolis, MN 55401

CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/918,411
 FILING DATE: 21-JUL-1992
 APPLICATION NUMBER: 08 07/746,254
 FILING DATE: 26-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: FROMMET, WILLIAM S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 45410-2440
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-3312
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 72 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-204-729 11

Query Match 65.08, Score 18.2, Pos 1, Pos 1, Pos 1, Pos 1
 Best Local Similarity 87.08; Prod. No. 18;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0

5 CTAGAGCCTCTTACGTCGAGG 27
 1111111111111111111111
 20 CTAGAGCCTCTCTGAGTCGAGG 42

RESULT 14
 US-08-204-729-10/2
 Sequence 10, Application US/08204729
 Patent No. 5658572
 GENERAL INFORMATION:
 APPLICANT: Pacetti, Enzo
 APPLICANT: Taylor, Jill
 TITLE OF INVENTION: INFECTIOUS BURSAL DISEASE VIRUS
 TITLE OF INVENTOR: RECOMBINANT EXVIRUS VACCINE
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CURTIS, MORRIS & SALTORI
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/07/204,729
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/746,254
 FILING DATE: 26-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: FROMMET, WILLIAM S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 45410-2440
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 72 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-204-729 10

Query Match 65.08, Score 18.2, Pos 1, Pos 1, Pos 1, Pos 1
 Best Local Similarity 87.08; Prod. No. 18;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0

5 CTAGAGCCTCTTACGTCGAGG 27
 1111111111111111111111
 20 CTAGAGCCTCTCTGAGTCGAGG 42

RESULT 14
 US-08-204-729 11
 Sequence 11, Application US/08204729
 Patent No. 5658572
 GENERAL INFORMATION:
 APPLICANT: Pacetti, Enzo
 APPLICANT: Taylor, Jill
 TITLE OF INVENTION: INFECTIOUS BURSAL DISEASE VIRUS
 TITLE OF INVENTOR: RECOMBINANT EXVIRUS VACCINE
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CURTIS, MORRIS & SALTORI
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/07/204,729
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/746,254
 FILING DATE: 26-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: FROMMET, WILLIAM S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 45410-2440
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 72 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-204-729 11
 Sequence 11, Application US/08204729
 Patent No. 5658572
 GENERAL INFORMATION:
 APPLICANT: Pacetti, Enzo
 APPLICANT: Taylor, Jill
 TITLE OF INVENTION: INFECTIOUS BURSAL DISEASE VIRUS
 TITLE OF INVENTOR: RECOMBINANT EXVIRUS VACCINE
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CURTIS, MORRIS & SALTORI
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/07/204,729
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/746,254
 FILING DATE: 26-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: FROMMET, WILLIAM S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 45410-2440
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 72 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-204-729 11
 Sequence 11, Application US/08204729
 Patent No. 5658572
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0

5 CTAGAGCCTCTTACGTCGAGG 27
 1111111111111111111111
 20 CTAGAGCCTCTCTGAGTCGAGG 42

RESULT 14
 US-08-204-729-10/2
 Sequence 10, Application US/08204729
 Patent No. 5658572
 GENERAL INFORMATION:
 APPLICANT: Pacetti, Enzo
 APPLICANT: Taylor, Jill
 TITLE OF INVENTION: INFECTIOUS BURSAL DISEASE VIRUS
 TITLE OF INVENTOR: RECOMBINANT EXVIRUS VACCINE
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CURTIS, MORRIS & SALTORI
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/07/204,729
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/746,254
 FILING DATE: 26-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: FROMMET, WILLIAM S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 45410-2440
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 72 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

Query Match 65.7% Score 18.4 Lb 4: Length 1416
 Best Local Similarity 79.6% Prod. No. 21
 Matches 22: Conservative 0: Mismatches 6: Indels 0: Gaps 0

UY 1 CGGTGACCTTAAGAACTTCAGAGG 28
 ||| ||||| || ||| ||||| ||
 Db 343 CGGCGACCTGACGACAGGTCTGAGG 316

RESULT 6
 US-09-252-991A-1512
 : Sequence 1512: Aff11-2716 us09252991A
 : Patent No. 6551795
 : GENERAL INFORMATION:
 : APPLICANT: Marc J. Rubenfield et al.
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 : FILE REFERENCE: 107196.136
 : CURRENT APPLICATION NUMBER: US/09/272 991A
 : PRIOR FILING DATE: 1999-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,798
 : PRIOR FILING DATE: 1998-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,190
 : NUMBER OF SEQ ID NOS: 33142
 : SEQ ID NO 1512
 : LENGTH: 1416
 : TYPE: DNA
 : ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-1512

Query Match 65.7% Score 18.4 Lb 4: Length 1416
 Best Local Similarity 79.6% Prod. No. 21
 Matches 22: Conservative 0: Mismatches 6: Indels 0: Gaps 0

UY 1 CGGTGACCTTAAGAACTTCAGAGG 28
 ||| ||||| || ||| ||||| ||
 Db 851 CGGCGACCTGACGACAGGTCTGAGG 878

RESULT 7
 US-09-252-991A-1464
 : Sequence 1464: Application us09252991A
 : Patent No. 6551795
 : GENERAL INFORMATION:
 : APPLICANT: Marc J. Rubenfield et al.
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 : FILE REFERENCE: 107196.136
 : CURRENT APPLICATION NUMBER: US/09/272 991A
 : PRIOR FILING DATE: 1999-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,798
 : PRIOR FILING DATE: 1998-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,190
 : NUMBER OF SEQ ID NOS: 33142
 : SEQ ID NO 1464
 : LENGTH: 2352
 : TYPE: DNA
 : ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-1464

Query Match 65.7% Score 18.4 Lb 4: Length 1416
 Best Local Similarity 79.6% Prod. No. 21
 Matches 22: Conservative 0: Mismatches 6: Indels 0: Gaps 0

UY 1 CGGTGACCTTAAGAACTTCAGAGG 28
 ||| ||||| || ||| ||||| ||
 Db 807 CGGCGACCTGACGACAGGTCTGAGG 834

RESULT 8
 US-09-252-991A-1663/C

: Sequence 1663: Application us09252991A
 : Patent No. 6551795
 : GENERAL INFORMATION:
 : APPLICANT: Marc J. Rubenfield et al.
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 : FILE REFERENCE: 107196.136
 : CURRENT APPLICATION NUMBER: US/09/272 991A
 : PRIOR FILING DATE: 1999-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,798
 : PRIOR FILING DATE: 1998-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,190
 : NUMBER OF SEQ ID NOS: 33142
 : SEQ ID NO 1663
 : LENGTH: 1420
 : TYPE: DNA
 : ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-1663

Query Match 65.7% Score 18.4 Lb 4: Length 1416
 Best Local Similarity 79.6% Prod. No. 21
 Matches 22: Conservative 0: Mismatches 6: Indels 0: Gaps 0

UY 1 CGGTGACCTTAAGAACTTCAGAGG 28
 ||| ||||| || ||| ||||| ||
 Db 1420 CGGCGACCTGACGACAGGTCTGAGG 1449

RESULT 9
 US-09-106-100-211
 : Sequence 211: Application us09106100
 : Patent No. 6413607
 : GENERAL INFORMATION:
 : APPLICANT: ProteoGenix, Inc.
 : TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
 : NUMBER OF SEQUENCES: 142
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: C/O ProteoGenix, Inc.
 : STREET: 60 Littleton Ave.
 : CITY: New York
 : STATE: NY
 : COUNTRY: USA
 : ZIP: 10046
 : CLASS: 10046
 : METHOD TYPE: Protein Risk
 : COMPOSITION: 100% ProteoGenix
 : INVENTOR: ProteoGenix, Inc.
 : ATTORNEY: ProteoGenix, Inc.
 : CURRENT FILING DATE: 1999-02-18
 : PRIOR FILING DATE: 1998-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,798
 : PRIOR FILING DATE: 1998-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,190
 : NUMBER OF SEQ ID NOS: 33142
 : SEQ ID NO 211
 : LENGTH: 211
 : TYPE: DNA
 : ORGANISM: Pseudomonas aeruginosa
 US-09-106-100-211


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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,311
FILING DATE: 21 JUL 1992
APPLICATION NUMBER: US 07/736,254
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2440
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-4333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ. ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-303-124-11

Query Match      65.0%  Score 18.4  Pos 1:  Length 72
Host Local Similarity 87.0%  Prod. No. 16
Matches 29:  Conservative  0,  Mismatches  4,  Indels  0,  Gaps  0

QY      2  CCGCAGCTTAAGAAATCTTCTG 24
DB      42  CCGCAGCTTAAGAAATCTTCTG 20

RESULT 14
US-08-204-729-10
Sequence 10: Affiliation: 07/09/92
Patent No. 5656572
GENERAL INFORMATION:
APPLICANT: Taylor, Jill
TITLE OF INVENTION: IMPATHOS BRESAL BISMAR VIRUS
TITLE OF INVENTION: RECOMBINANT EXVIRUS VACCINE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Corbis, Morris & Parrish
ADDRESS: 570 William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/09/92
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/07/96, 254
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-4333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

```

```

US-08-204-729-10

Query Match      65.0%  Score 18.4  Pos 1:  Length 72
Host Local Similarity 87.0%  Prod. No. 16
Matches 29:  Conservative  0,  Mismatches  4,  Indels  0,  Gaps  0

QY      2  CCGCAGCTTAAGAAATCTTCTG 24
DB      42  CCGCAGCTTAAGAAATCTTCTG 20

RESULT 14
US-08-204-729-10
Sequence 10: Affiliation: 07/09/92
Patent No. 5656572
GENERAL INFORMATION:
APPLICANT: Taylor, Jill
TITLE OF INVENTION: IMPATHOS BRESAL BISMAR VIRUS
TITLE OF INVENTION: RECOMBINANT EXVIRUS VACCINE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Corbis, Morris & Parrish
ADDRESS: 570 William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/09/92
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/07/96, 254
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-4333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-204-729-11

Query Match      65.0%  Score 18.4  Pos 1:  Length 72
Host Local Similarity 87.0%  Prod. No. 16
Matches 29:  Conservative  0,  Mismatches  4,  Indels  0,  Gaps  0

QY      2  CCGCAGCTTAAGAAATCTTCTG 24
DB      42  CCGCAGCTTAAGAAATCTTCTG 20

RESULT 15
US-08-475-064-28
Sequence 09: Affiliation: 07/09/92
Patent No. 5656572
GENERAL INFORMATION:
APPLICANT: Taylor, Jill
TITLE OF INVENTION: IMPATHOS BRESAL BISMAR VIRUS
TITLE OF INVENTION: RECOMBINANT EXVIRUS VACCINE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Corbis, Morris & Parrish
ADDRESS: 570 William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/09/92
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/07/96, 254
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-4333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

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TYPE: DNA
ORGANISM: Drosophila melanogaster
FEATURES:
OTHER INFORMATION: genomic map (no-translation product) (1)
OTHER INFORMATION: nucleotide sequence
US-09-492 912A-1

Query Match 65.4% Score 172 Db 4 Length 24500
Best Local Similarity 80.0% Prod. No. 451
Matches 40 Conserved 0 Mismatches 5 Indels 0 Gaps 0

QY 1 GCATATACGCTACGACCTTACGAC 25
|||||
ID 21923 GCATATACGCTACGACCTTACGAC 21899

RESULT 5
US-08-702-153-5

Sequence 5, Application US/0970915
Patent No. 5955332

GENERAL INFORMATION:

APPLICANT: PREVOTS, Fabrice

APPLICANT: TOLOU, Sandrine

TITLE OF INVENTION: Nucleic acid sequences and plasmids

TITLE OF INVENTION: Nucleic acid sequences and plasmids

TITLE OF INVENTION: Nucleic acid sequences and plasmids

TITLE OF INVENTION: Nucleic acid sequences and plasmids

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #10, Version #1.05

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/0970915

FILING DATE: 23-AUG-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95 09980

FILING DATE: 22-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16781/525

TELEPHONE: (202) 672-5390

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 5.

SEQUENCE CHARACTERISTICS:

LENGTH: 31 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOL-SCULE TYPE: DNA (genomic)

HYDROPHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: misc_signal

LOCATION: 6..11

OTHER INFORMATION: /function: "RanH1 restriction"

OTHER INFORMATION: /function: "RanH1 restriction"

OTHER INFORMATION: /function: "RanH1 restriction"

OTHER INFORMATION: /function: "RanH1 restriction"

OTHER INFORMATION: /function: "RanH1 restriction"

OTHER INFORMATION: /function: "RanH1 restriction"

OTHER INFORMATION: /function: "RanH1 restriction"

Query Match 65.4% Score 172 Db 4 Length 24500
Best Local Similarity 80.0% Prod. No. 451
Matches 40 Conserved 0 Mismatches 5 Indels 0 Gaps 0

QY 1 GCATATACGCTACGACCTTACGAC 25
|||||
ID 21923 GCATATACGCTACGACCTTACGAC 21899

RESULT 7
US-09-252-991A-1000

Sequence 1, Application US/0970915
Patent No. 5955332

GENERAL INFORMATION:

APPLICANT: PREVOTS, Fabrice

APPLICANT: TOLOU, Sandrine

TITLE OF INVENTION: Nucleic acid sequences and plasmids

TITLE OF INVENTION: Nucleic acid sequences and plasmids

TITLE OF INVENTION: Nucleic acid sequences and plasmids

TITLE OF INVENTION: Nucleic acid sequences and plasmids

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TITLE OF INVENTION: Nucleic acid sequences and plasmids

TITLE OF INVENTION: Nucleic acid sequences and plasmids

TITLE OF INVENTION: Nucleic acid sequences and plasmids

TITLE OF INVENTION: Nucleic acid sequences and plasmids

SOFTWARE: ASCII TEXT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 75,96,941,000
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Brookes, A. Anders
 REGISTRATION NUMBER: 35,373
 REFERENCE/AGENT NUMBER: FB349P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ. ID NO: 139:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 865 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-961-083-139

Query Match 61.5% Score 167 DB 3 Length 865
 Best Local Similarity 79.2% Seed No. 79
 Matches 19 Conserved 0 Mismatches 5 Indels 0 Gaps 0

QY 2 GTTGAAGTCTAGTGTATATG 25
 DB 652 GTTGAATTCTAGATTAATATG 629

RESULT 12
 US-09-536-784-139/G
 Sequence 139, Application US/66636784
 Patent No. 6573082
 GENPAT. INFORMATION:
 APPLICANT: Choi et. al.
 TITLE OF INVENTION: Strompococcus Pneumoniae Antigens and Vaccines
 NUMBER OF SEQUENCES: 452
 CORRESPONDENCE ADDRESS:
 ADDRESS: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS Version 6.22
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09-09-536-784
 FILING DATE: 20-09-1997
 CLASSIFICATION: unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/961,083
 FILING DATE: OCT-30-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Michelle S. Marks
 REGISTRATION NUMBER: 41,971
 REFERENCE/AGENT NUMBER: FB349P3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ. ID NO: 139:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 805 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 139:

US 09 536 784 139

Query Match 61.5% Score 167 DB 3 Length 865
 Best Local Similarity 79.2% Seed No. 79
 Matches 19 Conserved 0 Mismatches 5 Indels 0 Gaps 0

QY 2 GTTGAAGTCTAGTGTATATG 25
 DB 652 GTTGAATTCTAGATTAATATG 629

RESULT 13

PCT-US96-05420A 464

SEQUENCE 464, Application PCT/US96/05420A
 GENPAT. INFORMATION:
 APPLICANT: Human Genome Sciences
 APPLICANT: 9410 Key West Avenue
 APPLICANT: Rockville, MD 20850
 APPLICANT: United States of America
 APPLICANT: Johns Hopkins University
 APPLICANT: 720 Rutland Avenue
 APPLICANT: Baltimore, MD 21205
 APPLICANT: United States of America
 APPLICANT: Mark D. Adams
 APPLICANT: Green White
 APPLICANT: Hamilton Co. South
 TITLE OF INVENTION: Related to Sequence of the nucleotide
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESS: Steven K. Ross, et al., 1000
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-4944
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS Version 6.22
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/05420A
 FILING DATE: April 24, 1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/949,112
 FILING DATE: June 7, 1995
 APPLICATION DATA:
 APPLICATION NUMBER: 08/949,127
 FILING DATE: June 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Eric K. Strode
 REGISTRATION NUMBER: 36,098
 REFERENCE/AGENT NUMBER: 14-09-0110-06
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2544
 INFORMATION FOR SEQ. ID NO: 146:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 875 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 PCT-US96-05420A-464

Query Match 61.5% Score 167 DB 3 Length 865
 Best Local Similarity 79.2% Seed No. 79
 Matches 19 Conserved 0 Mismatches 5 Indels 0 Gaps 0

QY 2 GTTGAAGTCTAGTGTATATG 25
 DB 652 GTTGAATTCTAGATTAATATG 629

INVENTOR: CHAWA, THEODORE
 TYPE: NOVELTY
 CLASSIFICATION: E01C 1/00
 FIELD OF INVENTION: LAMP
 TITLE: LAMP

2002-04-14
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INVENTOR: CHAWA, THEODORE
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US-10-288-930-1/0
 ? Sequence 1, Application US/0208030
 ? Publication No. US2003012822A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Glenn, Matthew
 ? APPLICANT: Inubers, Mark W
 ? APPLICANT: Dekker, James
 ? TITLE OF INVENTION: Poly-oligo-oligos and polypeptides, methods for incorporating
 ? FILE REFERENCE: 11000 10480161
 ? CURRENT FILING DATE: 2002-11-05
 ? PRIOR APPLICATION NUMBER: 09/721,622
 ? PRIOR FILING DATE: 2000 11 28
 ? PRIOR APPLICATION NUMBER: 60/418,801
 ? PRIOR FILING DATE: 1999-12-02
 ? NUMBER OF SEQ ID NOS: 124
 ? SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO 1
 ? LENGTH: 711
 ? TYPE: DNA
 ? ORGANISM: Lactobacillus rhamnosus
 US-10-288-930-1

Query Match 65.4%; Score 17; DB 12; Length 711;
 Best Local Similarity 80.0%; Pred. No. 2,3e-02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CATTGAACTGCTAGCTATGATG 25
 DB 465 CATTGAACTGCTAGCTATGATG 441

RESULT 13

US-09-822-849A-247
 ? Sequence 247, Application US/9922849A
 ? Patent No. US20020045170A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Wong, Gordon G.
 ? APPLICANT: Clark, Hilary
 ? APPLICANT: Freichel, Kim
 ? APPLICANT: Agostino, Michael J.
 ? APPLICANT: Howes, Steven H.
 ? APPLICANT: Resnick, Richard J.
 ? APPLICANT: Gulukota, Kamalakar
 ? APPLICANT: Graham, James R.
 ? APPLICANT: Genetics Institute, Inc.
 ? TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
 ? FILE REFERENCE: GIN 6403
 ? CURRENT APPLICATION NUMBER: US/9922849A
 ? CURRENT FILING DATE: 2001-09-04
 ? PRIOR APPLICATION NUMBER: 60/195,582
 ? PRIOR FILING DATE: 2000-04-05
 ? NUMBER OF SEQ ID NOS: 598
 ? SOFTWARE: Patent In Ver. 2.0
 ? SEQ ID NO 247
 ? LENGTH: 2254
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US-09-822-849A-247

Query Match 65.4%; Score 17; DB 9; Length 2254;
 Best Local Similarity 90.0%; Pred. No. 2,9e-02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CATTGAACTGCTAGCTATGATG 25
 DB 563 CATTGAACTGCTAGCTATGATG 587

RESULT 14

US-09-764-891-9927/0
 ? Sequence 9927, Application US/99764891
 ? Publication No. US2003007668A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Kosco et al.
 ? TITLE OF INVENTION: Methods for the detection and identification
 ? FILE REFERENCE: 18006
 ? CURRENT APPLICATION NUMBER: US/99764891
 ? CURRENT FILING DATE: 2001-01-17
 ? PRIOR APPLICATION DATA REMOVED - CONSULT PAM OF FILE WRAPPER
 ? NUMBER OF SEQ ID NOS: 19211
 ? SOFTWARE: Patent In Ver. 2.0
 ? SEQ ID NO 9927
 ? LENGTH: 22237
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US-09-764-891-9927

Query Match 65.4%; Score 17; DB 13; Length 22237;
 Best Local Similarity 80.0%; Pred. No. 4,6e-02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 1;

QY 2 CTTGAACTGCTAGCTATGATG 25
 DB 564 CTTGAACTGCTAGCTATGATG 500

RESULT 15

US-09-764-891-9927/0
 ? Sequence 9926, Application US/99764891
 ? Publication No. US2003007668A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Kosco et al.
 ? TITLE OF INVENTION: Methods for the detection and identification
 ? FILE REFERENCE: 18006
 ? CURRENT APPLICATION NUMBER: US/99764891
 ? CURRENT FILING DATE: 2001-01-17
 ? PRIOR APPLICATION DATA REMOVED - CONSULT PAM OF FILE WRAPPER
 ? NUMBER OF SEQ ID NOS: 19211
 ? SOFTWARE: Patent In Ver. 2.0
 ? SEQ ID NO 9926
 ? LENGTH: 22238
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US-09-764-891-9926

Query Match 65.4%; Score 17; DB 11; Length 22238;
 Best Local Similarity 80.0%; Pred. No. 4,6e-02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 1;

QY 2 CTTGAACTGCTAGCTATGATG 25
 DB 565 CTTGAACTGCTAGCTATGATG 501

Search completed: August 14, 2003, 09:09:36
 Job Time: 112.152 secs



GenProbe version 5.1.6
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nm nucleotide - nucleotide search, using sw model

Run on: August 14, 2003, 02:19:25, Search time 13m 11s 18.00s

(without alignment)
141,016 Million cell updates/sec

Title: US-10-009-962-1

Sequence: 1 CCCCGAGAGAGTTCCTTAAAGGTGACGCG 24

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Search: 1504479 seqs, 118970152 residues

Total number of hits satisfying chosen parameters: 3089 hits

Minimum E# seq length: 0

Maximum E# seq length: 200000000

Post-processing: Minimum Match 98

Listing first 45 summaries

Database: Published Applications_NA*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	24	100.0	28	13	US-10-09-962-1
3	19.6	70.0	245	10	US-09-878-524 7664
4	19.6	70.0	251	10	US-09-878-524 7664
5	19.6	70.0	228	10	US-09-878-524 7664
6	19.6	70.0	212	9	US-09-927-611A 7
7	19.6	70.0	212	9	US-09-927-611A 7
8	19.6	70.0	212	9	US-09-927-611A 7
9	19.6	70.0	212	9	US-09-927-611A 7
10	18.8	67.1	299	10	US-09-927-611A 7
11	18.8	67.1	299	10	US-09-927-611A 7
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13	18.8	67.1	299	10	US-09-927-611A 7
14	18.8	67.1	299	10	US-09-927-611A 7
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23	18	64.3	1300	10	US-09-927-611A 7
24	18	64.3	1300	10	US-09-927-611A 7
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27	17.6	62.9	600	9	US-09-927-611A 7
28	17.6	62.9	600	9	US-09-927-611A 7
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36	17.6	62.9	600	9	US-09-927-611A 7
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US-09-878-574-13495/C
 ? Sequence 1495, Application US/09078574
 ? Patent No. US20020110548A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Byrum, Joseph R.
 ? APPLICANT: La Rosa, Thomas J.
 ? APPLICANT: Thompson, Michael D.
 ? TITLE OF INVENTION: Nucleic Acid Molecules and Uses in Detecting and Treating
 ? FILE OF INVENTION: Plants
 ? FILE REFERENCE: 38-21(1540)B
 ? CURRENT APPLICATION NUMBER: US/09/078574
 ? CURRENT FILING DATE: 2001-12-21
 ? PRIOR APPLICATION NUMBER: 09/733,535
 ? PRIOR FILING DATE: 1999-06-14
 ? NUMBER OF SEQ ID NOS: 15775
 ? SEQ ID No: 1495
 ? LENGTH: 278
 ? TYPE: DNA
 ? ORGANISM: Glycine max
 ? OTHER INFORMATION: Cloned In: 701957265H1
 US-09-878-574-13495

Query Match: 70.0% Score 19.6% DB Len: 16,000,000
 Best Local Similarity: 84.6% Pred. No: 12
 Matches: 22 Constructed from 0 Results: 1 to 1000's

US-09-927-616A-1/C

? Sequence 1, Application US/09027616A
 ? Patent No. US2002009034A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Triplett, Eric W
 ? APPLICANT: Herliach, Thomas G.
 ? TITLE OF INVENTION: Biological Control of Crown Gall Disease
 ? FILE REFERENCE: 960256 9273
 ? CURRENT APPLICATION NUMBER: US/09/927,616A
 ? CURRENT FILING DATE: 2001-11-02
 ? PRIOR APPLICATION NUMBER: 60/224,626
 ? PRIOR FILING DATE: 2000-08-11
 ? NUMBER OF SEQ ID NOS: 9
 ? SOFTWARE: Patentin Ver. 2.1
 ? SEQ ID No: 1
 ? LENGTH: 7142
 ? TYPE: DNA
 ? ORGANISM: Nucleotide sequence for 1413 141
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: (597)..(722)
 ? OTHER INFORMATION: t1x8 coding sequence
 ? NAME/KEY: CDS
 ? LOCATION: (794)..(1912)
 ? OTHER INFORMATION: t1x8 coding sequence
 ? NAME/KEY: CDS
 ? LOCATION: (2982)..(4229)
 ? OTHER INFORMATION: t1x8 coding sequence
 ? NAME/KEY: CDS
 ? LOCATION: (4968)..(5741)
 ? OTHER INFORMATION: t1x8 coding sequence
 ? NAME/KEY: CDS
 ? LOCATION: (5996)..(6778)
 ? OTHER INFORMATION: t1x8 coding sequence
 US-09-927-616A-1

Query Match: 70.0% Score 19.6% DB Len: 16,000,000
 Best Local Similarity: 84.6% Pred. No: 12
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US-09-927-616A-1/C

? Sequence 1, Application US/09027616A
 ? Patent No. US2002009034A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Triplett, Eric W
 ? APPLICANT: Herliach, Thomas G.
 ? TITLE OF INVENTION: Biological Control of Crown Gall Disease
 ? FILE REFERENCE: 960256 9273
 ? CURRENT APPLICATION NUMBER: US/09/927,616A
 ? CURRENT FILING DATE: 2001-11-02
 ? PRIOR APPLICATION NUMBER: 60/224,626
 ? PRIOR FILING DATE: 2000-08-11
 ? NUMBER OF SEQ ID NOS: 9
 ? SOFTWARE: Patentin Ver. 2.1
 ? SEQ ID No: 1
 ? LENGTH: 7142
 ? TYPE: DNA
 ? ORGANISM: Nucleotide sequence for 1413 141
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: (597)..(722)
 ? OTHER INFORMATION: t1x8 coding sequence
 ? NAME/KEY: CDS
 ? LOCATION: (794)..(1912)
 ? OTHER INFORMATION: t1x8 coding sequence
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 US-09-927-616A-1

Query Match: 70.0% Score 19.6% DB Len: 16,000,000
 Best Local Similarity: 84.6% Pred. No: 12
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US-09-927-616A-1/C

? Sequence 1, Application US/09027616A
 ? Patent No. US2002009034A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Triplett, Eric W
 ? APPLICANT: Herliach, Thomas G.
 ? TITLE OF INVENTION: Biological Control of Crown Gall Disease
 ? FILE REFERENCE: 960256 9273
 ? CURRENT APPLICATION NUMBER: US/09/927,616A
 ? CURRENT FILING DATE: 2001-11-02
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 ? LOCATION: (5996)..(6778)
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 US-09-927-616A-1


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RESULT 12
US-09-738-626-1692
: Sequence 1692, Application US/9738626
: Publication No. US20020197605A1
: GENERAL INFORMATION:
: APPLICANT: NAKAGAWA, SATOSHI
: APPLICANT: MIZOGUCHI, HIROSHI
: APPLICANT: AMDO, SEIKO
: APPLICANT: HAYASHI, MIKIO
: APPLICANT: OCHIAI, KEIKO
: APPLICANT: YOKOI, HARUHIKO
: APPLICANT: TATEISHI, NOBOKO
: APPLICANT: SENO, AKIHITO
: APPLICANT: IKEDA, MASARO
: APPLICANT: OZAKI, AKIO
: TITLE OF INVENTION: NOVEL PEPTIDE/OLIGOPEPTIDES
: FILE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: 05/9738626
: PRIOR FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/777184
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: JP 2001/59182
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 99/299938
: PRIOR FILING DATE: 2000-09-03
: NUMBER OF SEQ ID NOS: 7059
: SOFTWARE: Patent In Ver. 3.0
: SEQ ID NO: 1692
: LENGTH: 1296
: TYPE: DNA
: ORGANISM: Corynebacterium glutamicum
US-09-738-626-1692

Query Match 65.08; Score 18.2; Len 10; Length 1296;
Best Local Similarity 87.08; Pred. No. 67;
Matches 20; Conserved 100; Mismatches 0;

CY 2 CCGGAGACGCTTCTAGCTG 24
ID 622 CCGGAGACGCTTCTAGCTG 844

RESULT 13
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: Sequence 1692, Application US/9738626
: Publication No. US20020197605A1
: GENERAL INFORMATION:
: APPLICANT: NAKAGAWA, SATOSHI
: APPLICANT: MIZOGUCHI, HIROSHI
: APPLICANT: AMDO, SEIKO
: APPLICANT: HAYASHI, MIKIO
: APPLICANT: OCHIAI, KEIKO
: APPLICANT: YOKOI, HARUHIKO
: APPLICANT: TATEISHI, NOBOKO
: APPLICANT: SENO, AKIHITO
: APPLICANT: IKEDA, MASARO
: APPLICANT: OZAKI, AKIO
: TITLE OF INVENTION: NOVEL PEPTIDE/OLIGOPEPTIDES
: FILE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: 05/9738626
: PRIOR FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/777184
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: JP 2001/59182
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 99/299938
: PRIOR FILING DATE: 2000-09-03
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: TYPE: DNA
: ORGANISM: Corynebacterium glutamicum
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: Sequence 1692, Application US/9738626
: Publication No. US20020197605A1
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: APPLICANT: NAKAGAWA, SATOSHI
: APPLICANT: MIZOGUCHI, HIROSHI
: APPLICANT: AMDO, SEIKO
: APPLICANT: HAYASHI, MIKIO
: APPLICANT: OCHIAI, KEIKO
: APPLICANT: YOKOI, HARUHIKO
: APPLICANT: TATEISHI, NOBOKO
: APPLICANT: SENO, AKIHITO
: APPLICANT: IKEDA, MASARO
: APPLICANT: OZAKI, AKIO
: TITLE OF INVENTION: NOVEL PEPTIDE/OLIGOPEPTIDES
: FILE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: 05/9738626
: PRIOR FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/777184
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: JP 2001/59182
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 99/299938
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: SOFTWARE: Patent In Ver. 3.0
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: LENGTH: 1296
: TYPE: DNA
: ORGANISM: Corynebacterium glutamicum
US-09-738-626-1692

Query Match 65.08; Score 18.2; Len 10; Length 1296;
Best Local Similarity 87.08; Pred. No. 67;
Matches 20; Conserved 100; Mismatches 0;

CY 2 CCGGAGACGCTTCTAGCTG 24
ID 622 CCGGAGACGCTTCTAGCTG 844

RESULT 14
US-09-878-624-8642/0
: Sequence 8642, Application US/9738626
: Publication No. US20020197605A1
: GENERAL INFORMATION:
: APPLICANT: Thompson, Michael L.
: APPLICANT: Thompson, Michael L.
: TITLE OF INVENTION: NOVEL PEPTIDE/OLIGOPEPTIDES
: FILE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: 05/9738626
: PRIOR FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/777184
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: JP 2001/59182
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 99/299938
: PRIOR FILING DATE: 2000-09-03
: NUMBER OF SEQ ID NOS: 7059
: SOFTWARE: Patent In Ver. 3.0
: SEQ ID NO: 8642
: LENGTH: 1296
: TYPE: DNA
: ORGANISM: Corynebacterium glutamicum
US-09-878-624-8642/0

Query Match 65.08; Score 18.2; Len 10; Length 1296;
Best Local Similarity 87.08; Pred. No. 67;
Matches 20; Conserved 100; Mismatches 0;

CY 2 CCGGAGACGCTTCTAGCTG 24
ID 622 CCGGAGACGCTTCTAGCTG 844

RESULT 15
US-09-878-624-8642/0
: Sequence 8642, Application US/9738626
: Publication No. US20020197605A1
: GENERAL INFORMATION:
: APPLICANT: Thompson, Michael L.
: APPLICANT: Thompson, Michael L.
: TITLE OF INVENTION: NOVEL PEPTIDE/OLIGOPEPTIDES
: FILE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: 05/9738626
: PRIOR FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/777184
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: JP 2001/59182
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 99/299938
: PRIOR FILING DATE: 2000-09-03
: NUMBER OF SEQ ID NOS: 7059
: SOFTWARE: Patent In Ver. 3.0
: SEQ ID NO: 8642
: LENGTH: 1296
: TYPE: DNA
: ORGANISM: Corynebacterium glutamicum
US-09-878-624-8642/0

Query Match 65.08; Score 18.2; Len 10; Length 1296;
Best Local Similarity 87.08; Pred. No. 67;
Matches 20; Conserved 100; Mismatches 0;

CY 2 CCGGAGACGCTTCTAGCTG 24
ID 622 CCGGAGACGCTTCTAGCTG 844

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us-10-009-962-1.rnpb

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[illegible]

Continued Fraction Approximation

RESULT 12

US-09-738-626-1692/c
 ? Sequence 1692, Application No/99729679
 ? Publication No. US20000197605A1
 ? GENERAL INFORMATION:
 ? APPLICANT: NAKAGAWA, SATOSHI
 ? APPLICANT: MIZOGUCHI, HIROSHI
 ? APPLICANT: ANDO, SEIKO
 ? APPLICANT: HAYASHI, MARIKO
 ? APPLICANT: OCHIAI, KEIKO
 ? APPLICANT: YOKOI, HARUHIKO
 ? APPLICANT: TATEISHI, NAOKO
 ? APPLICANT: SENDU, AKIHIRO
 ? APPLICANT: IKEDA, MASATO
 ? APPLICANT: OZAKI, AKIO
 ? TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ? FILE REFERENCE: 249-125
 ? CURRENT APPLICATION NUMBER: JP 00/727784
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 2000-04-07
 ? PRIOR FILING DATE: 2000-04-07
 ? PRIOR FILING DATE: 2000-08-04
 ? NUMBER OF SEQ ID NOS: 7059
 ? SOFTWARE: Patentln ver. 3.0
 ? SEQ ID NO: 1692
 ? LENGTH: 1296
 ? TYPE: DNA
 ? ORGANISM: Corynebacterium glutamicum
 ? US-09-738-626-1692

Query Match 65.0%; Score 18.2; DB 1; Length 1296;
 Best Local Similarity 87.0%; Pred. No. 67;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

US 5 GAGCTTAAAGAGCTTGGAGG 27
 db 844 GAGCTTAAAGAGCTTGGAGG 822

RESULT 13

US-09-738-626-1
 ? Sequence 1, Application No/99729679
 ? Publication No. US20000197605A1
 ? GENERAL INFORMATION:
 ? APPLICANT: NAKAGAWA, SATOSHI
 ? APPLICANT: MIZOGUCHI, HIROSHI
 ? APPLICANT: ANDO, SEIKO
 ? APPLICANT: HAYASHI, MARIKO
 ? APPLICANT: OCHIAI, KEIKO
 ? APPLICANT: YOKOI, HARUHIKO
 ? APPLICANT: TATEISHI, NAOKO
 ? APPLICANT: SENDU, AKIHIRO
 ? APPLICANT: IKEDA, MASATO
 ? APPLICANT: OZAKI, AKIO
 ? TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ? FILE REFERENCE: 249-125
 ? CURRENT APPLICATION NUMBER: JP 00/727784
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 2000-04-07
 ? PRIOR FILING DATE: 2000-04-07
 ? PRIOR FILING DATE: 2000-08-04
 ? NUMBER OF SEQ ID NOS: 7059
 ? SOFTWARE: Patentln ver. 3.0
 ? SEQ ID NO: 1
 ? LENGTH: 3309400

TYPE: DNA
 ORGANISM: Corynebacterium glutamicum
 US-09-738-626-1

Query Match 65.0%; Score 18.2; DB 1; Length 1296;
 Best Local Similarity 87.0%; Pred. No. 67;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

US 5 GAGCTTAAAGAGCTTGGAGG 27
 db 844 GAGCTTAAAGAGCTTGGAGG 822

RESULT 14

US-09-878-574-8642
 ? Sequence 8642, Application No/0006974
 ? Publication No. US2000211949A1
 ? GENERAL INFORMATION:
 ? APPLICANT: KYOKKO, JUSEI
 ? APPLICANT: KYOKKO, JUSEI
 ? APPLICANT: KYOKKO, JUSEI
 ? APPLICANT: KYOKKO, JUSEI
 ? TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ? FILE REFERENCE: 38-21(1)101b
 ? CURRENT APPLICATION NUMBER: JP 00/727784
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 2000-04-07
 ? PRIOR FILING DATE: 2000-04-07
 ? PRIOR FILING DATE: 2000-08-04
 ? NUMBER OF SEQ ID NOS: 7059
 ? SOFTWARE: Patentln ver. 3.0
 ? SEQ ID NO: 8642
 ? LENGTH: 228
 ? TYPE: DNA
 ? ORGANISM: Mycobacterium
 ? US-09-878-574-8642

Query Match 65.0%; Score 18.2; DB 1; Length 228;
 Best Local Similarity 87.0%; Pred. No. 67;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

US 2 CTTTAAAGAGCTTGGAGG 27
 db 844 GAGCTTAAAGAGCTTGGAGG 822

RESULT 15

US-09-878-574-8642
 ? Sequence 8642, Application No/0006974
 ? Publication No. US2000211949A1
 ? GENERAL INFORMATION:
 ? APPLICANT: KYOKKO, JUSEI
 ? APPLICANT: KYOKKO, JUSEI
 ? APPLICANT: KYOKKO, JUSEI
 ? APPLICANT: KYOKKO, JUSEI
 ? TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ? FILE REFERENCE: 38-21(1)101b
 ? CURRENT APPLICATION NUMBER: JP 00/727784
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR FILING DATE: 2000-04-07
 ? PRIOR FILING DATE: 2000-04-07
 ? PRIOR FILING DATE: 2000-08-04
 ? NUMBER OF SEQ ID NOS: 7059
 ? SOFTWARE: Patentln ver. 3.0
 ? SEQ ID NO: 8642
 ? LENGTH: 287
 ? TYPE: DNA
 ? ORGANISM: Mycobacterium
 ? US-09-878-574-8642

Query Match 65.0%; Score 18.2; DB 1; Length 287;
 Best Local Similarity 87.0%; Pred. No. 67;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

US 2 CTTTAAAGAGCTTGGAGG 27
 db 844 GAGCTTAAAGAGCTTGGAGG 822

Thu Aug 14 09:09:37 2003

us-10-009-962-2.rnpb

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File: C:\Program Files\Internet Explorer\Internet Explorer.exe
Description: Internet Explorer
File Name: C:\Program Files\Internet Explorer\Internet Explorer.exe

Database version 5.1.6
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AM nucleic nucleic search, using SW model

Run on: August 14, 2003, 02:19:26, Search time 106.852 seconds
(without alignment)
14,016 Million cell updates/sec

Title: US-10-009-962-4

Perfect score: 26
Sequence: 1 GCATTATCAGCTACGACITGCAGAC 26

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1504479 seqs, 118970152 residues

Total number of hits satisfying chosen parameters: 4000768

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 98
Maximum Match 100%
Listing first 45 summaries

Database: Published_Applications_NA*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Job ID	Description
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11	26	100.0	26	US-10-009-962-4	Sequence 11, Affix
12	26	100.0	26	US-10-009-962-4	Sequence 12, Affix
13	26	100.0	26	US-10-009-962-4	Sequence 13, Affix
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ALL SUMMARIES

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RECORD: F SEQ ID NOS: 15775
 SEQ ID NO: 4804
 LENGTH: 473
 TYPE: DNA
 ORGANISM: glycine max
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)-(473)
 OTHER INFORMATION: unsure at all n locations
 US-10-027-632-4804

Query Match
 Best Local Similarity: 83.3% Prod. No.: 110-027
 Match: 29 Conserved: 29 Mismatches: 18 Indels: 0 Gap: 0

QY 1 CATTAATCAGCTAGCTGCAAC 24
 LB 13 CATTAATCAGCTAGCTGCAAC 36

RESULT 5
 US-10-016-157A-52
 Sequence: 52, Application: 3571001157A
 Publication No.: US2002019222A1
 GENERAL INFORMATION:
 APPLICANT: Sun, Yoonming
 APPLICANT: Ghosh, Malavika
 APPLICANT: Jhu, Chengsua
 TITLE OF INVENTION: Compositions and Methods relating to Colon Specific Green and Red
 FILE REFERENCE: DEX-0253
 CURRENT APPLICATION NUMBER: US 2001-10-21
 PRIOR APPLICATION NUMBER: US 60/244,717
 PRIOR FILING DATE: 2000-10-11
 NUMBER OF SEQ ID NOS: 250
 SOFTWARE: Patent version 3.1
 SEQ ID NO: 52
 LENGTH: 590
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-016-157A-52

Query Match
 Best Local Similarity: 83.3% Prod. No.: 110-027
 Matches: 29 Conserved: 29 Mismatches: 18 Indels: 0 Gap: 0

QY 2 CATTAATCAGCTAGCTGCAAC 25
 LB 519 CATTAATCAGCTAGCTGCAAC 542

RESULT 6
 US-10-027-632-182822C
 Sequence: 182822, Application: 65710027632
 GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 FILE REFERENCE: 108827-129
 CURRENT APPLICATION NUMBER: US 2002-04-30
 PRIOR APPLICATION NUMBER: US 60/218,006
 PRIOR FILING DATE: 2000-07-12
 PRIOR APPLICATION NUMBER: US 60/198,676
 PRIOR FILING DATE: 2000-04-20
 PRIOR APPLICATION NUMBER: US 60/194,484
 PRIOR FILING DATE: 2000-03-28
 PRIOR APPLICATION NUMBER: US 60/185,718
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: US 60/167,864
 PRIOR FILING DATE: 1999-11-24

RECORD: F SEQ ID NOS: 15775
 SEQ ID NO: 4804
 LENGTH: 473
 TYPE: DNA
 ORGANISM: glycine max
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)-(473)
 OTHER INFORMATION: unsure at all n locations
 US-10-027-632-4804

Query Match
 Best Local Similarity: 83.3% Prod. No.: 110-027
 Match: 29 Conserved: 29 Mismatches: 18 Indels: 0 Gap: 0

QY 1 CATTAATCAGCTAGCTGCAAC 24
 LB 13 CATTAATCAGCTAGCTGCAAC 36

RESULT 7
 US-10-027-632-182822C
 Sequence: 182822, Application: 65710027632
 GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 FILE REFERENCE: 108827-129
 CURRENT APPLICATION NUMBER: US 2002-04-30
 PRIOR APPLICATION NUMBER: US 60/218,006
 PRIOR FILING DATE: 2000-07-12
 PRIOR APPLICATION NUMBER: US 60/198,676
 PRIOR FILING DATE: 2000-04-20
 PRIOR APPLICATION NUMBER: US 60/194,484
 PRIOR FILING DATE: 2000-03-28
 PRIOR APPLICATION NUMBER: US 60/185,718
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: US 60/167,864
 PRIOR FILING DATE: 1999-11-24

Query Match
 Best Local Similarity: 83.3% Prod. No.: 110-027
 Matches: 29 Conserved: 29 Mismatches: 18 Indels: 0 Gap: 0

QY 2 CATTAATCAGCTAGCTGCAAC 25
 LB 519 CATTAATCAGCTAGCTGCAAC 542

RESULT 8
 US-10-027-632-182822C
 Sequence: 182822, Application: 65710027632
 GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 FILE REFERENCE: 108827-129
 CURRENT APPLICATION NUMBER: US 2002-04-30
 PRIOR APPLICATION NUMBER: US 60/218,006
 PRIOR FILING DATE: 2000-07-12
 PRIOR APPLICATION NUMBER: US 60/198,676
 PRIOR FILING DATE: 2000-04-20
 PRIOR APPLICATION NUMBER: US 60/194,484
 PRIOR FILING DATE: 2000-03-28
 PRIOR APPLICATION NUMBER: US 60/185,718
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: US 60/167,864
 PRIOR FILING DATE: 1999-11-24

RESULT 12

US-10-288-930-1
 ? Sequence 12: Application No. US20020139822A1
 ? PUBLICATION NO. US20020139822A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Glenn, Matthew
 ? APPLICANT: Lubberts, Mark W
 ? TITLE OF INVENTION: Polymers, lactides and poly(l-lactides) and poly(l-lactides) for use in drug delivery
 ? FILE REFERENCE: 11000.104861c1
 ? CURRENT APPLICATION NUMBER: 02/020202
 ? PRIOR FILING DATE: 2000-11-28
 ? PRIOR APPLICATION NUMBER: 60/443,801
 ? NUMBER OF SEQ ID NOS: 124
 ? SOFTWARE: FASTSEQ for Windows Version 4.0
 ? SEQ ID NO: 1
 ? LENGTH: 711
 ? TYPE: DNA
 ? ORGANISM: Lactobacillus rhamnosus
 US-10-288-930-1

Query Match: 65.4%; Score 17; Db 12; Length 711

Best Local Similarity: 80.0%; Prod. No. 2,400,02

Matches: 20; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0

US 2 CATTAATGAGTAACTGCAATG 26

Db 441 CATATCTCAAGCACTGCAATG 465

RESULT 13

US-09-822-819A-247/2
 ? Sequence 247: Application No. US20020045170A1
 ? Patent No. US20020045170A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Wong, Gordon C.
 ? APPLICANT: Clark, Hilary
 ? APPLICANT: Frechuel, Kim
 ? APPLICANT: Apostolov, Michael J.
 ? APPLICANT: Howes, Steven H.
 ? APPLICANT: Ruslock, Richard J.
 ? APPLICANT: Gulakota, Kamalakar
 ? APPLICANT: Graham, James R.
 ? TITLE OF INVENTION: POLYMERIZED EPOXY RESIN N-VEL SPECTED PROTEINS
 ? FILE REFERENCE: GIN 6403
 ? CURRENT APPLICATION NUMBER: 02/020202
 ? PRIOR FILING DATE: 2001-07-04
 ? PRIOR APPLICATION NUMBER: 60/195,582
 ? NUMBER OF SEQ ID NOS: 598
 ? SOFTWARE: PatentIn Ver. 2.0
 ? SEQ ID NO: 247
 ? LENGTH: 2254
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US-09-822-819A-247

Query Match: 65.4%; Score 17; Db 13; Length 2254

Best Local Similarity: 80.0%; Prod. No. 2,400,02

Matches: 20; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0

US 2 CATTAATGAGTAACTGCAATG 26

Db 587 CATAAAGAGTAACTGCAATG 564

RESULT 14

US-09-764-891-9927
 ? Sequence 9927: Application No. US20020045170A1
 ? PUBLICATION NO. US20020045170A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Rosson, et al.
 ? TITLE OF INVENTION: Nucleic acids, proteins, and antibodies
 ? FILE REFERENCE: 10000.104861c1
 ? CURRENT APPLICATION NUMBER: 02/020202
 ? PRIOR FILING DATE: 2001-07-04
 ? PRIOR APPLICATION NUMBER: 60/195,582
 ? NUMBER OF SEQ ID NOS: 1000
 ? SOFTWARE: PatentIn Ver. 2.0
 ? SEQ ID NO: 9927
 ? LENGTH: 2254
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US-09-764-891-9927

Query Match: 65.4%; Score 17; Db 14; Length 2254

Best Local Similarity: 80.0%; Prod. No. 2,400,02

Matches: 20; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0

US 2 CATTAATGAGTAACTGCAATG 26

Db 587 CATAAAGAGTAACTGCAATG 564

RESULT 15

US-09-764-891-9926
 ? Sequence 9926: Application No. US20020045170A1
 ? PUBLICATION NO. US20020045170A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Rosson, et al.
 ? TITLE OF INVENTION: Nucleic acids, proteins, and antibodies
 ? FILE REFERENCE: 10000.104861c1
 ? CURRENT APPLICATION NUMBER: 02/020202
 ? PRIOR FILING DATE: 2001-07-04
 ? PRIOR APPLICATION NUMBER: 60/195,582
 ? NUMBER OF SEQ ID NOS: 1000
 ? SOFTWARE: PatentIn Ver. 2.0
 ? SEQ ID NO: 9926
 ? LENGTH: 2254
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US-09-764-891-9926

Query Match: 65.4%; Score 17; Db 15; Length 2254

Best Local Similarity: 80.0%; Prod. No. 2,400,02

Matches: 20; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0

US 2 CATTAATGAGTAACTGCAATG 26

Db 587 CATAAAGAGTAACTGCAATG 564

Search completed: August 14, 2003 09:09:38
 Job Time: 414.852 secs

